CONFIDENTIAL

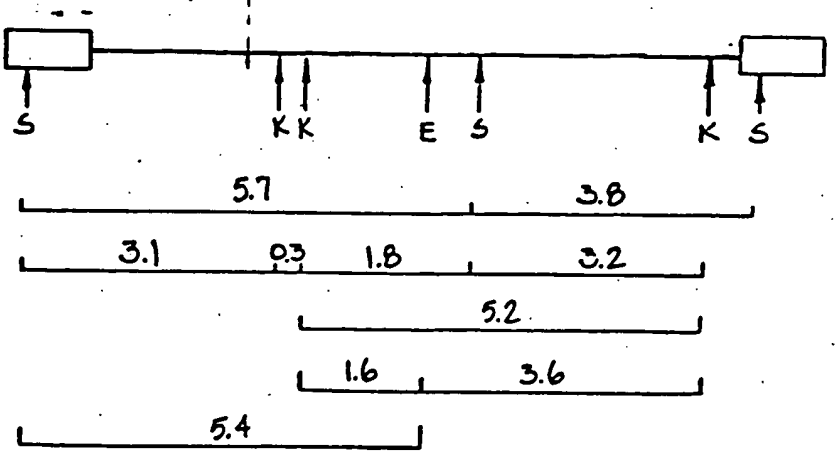



FIG. 1.

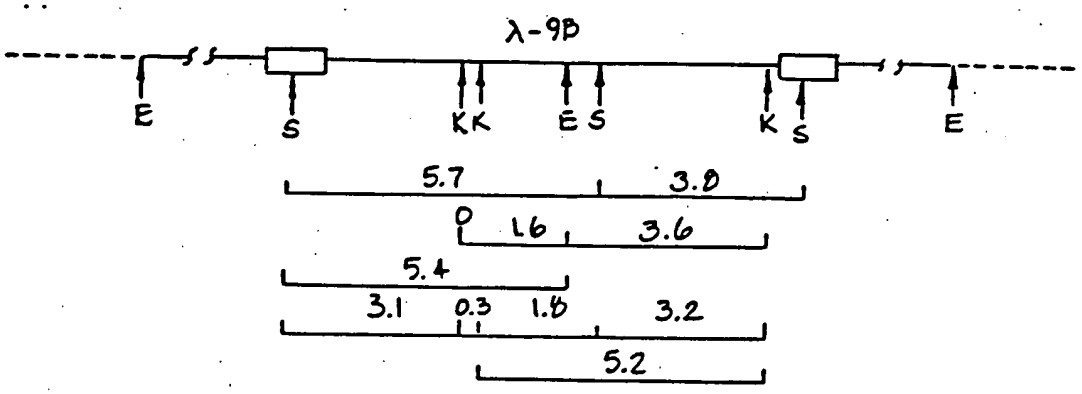



FIG. 2.

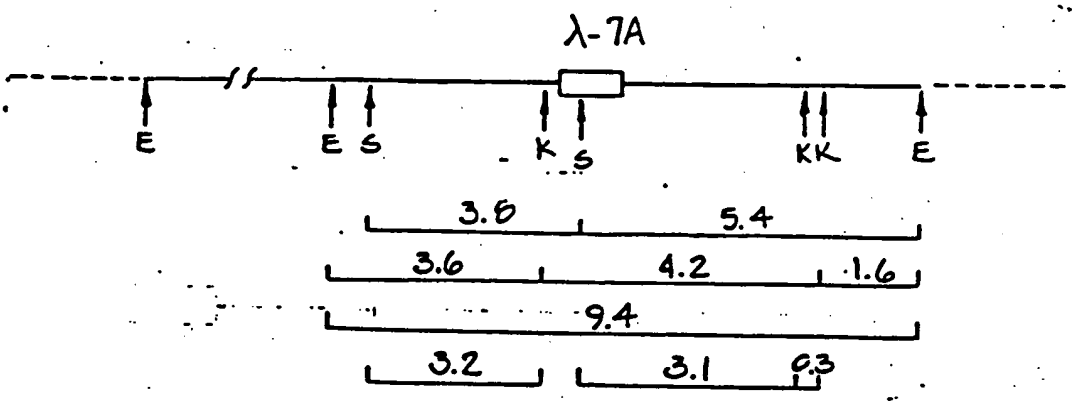



FIG. 3.

CONFIDENTIAL

on Oct 29 14:16:11 1984

Argument Map in DNA Strand ssarv2
from the '/v/lib/6mers' file.
Translation shown at open reading frames.

FIGURE 4

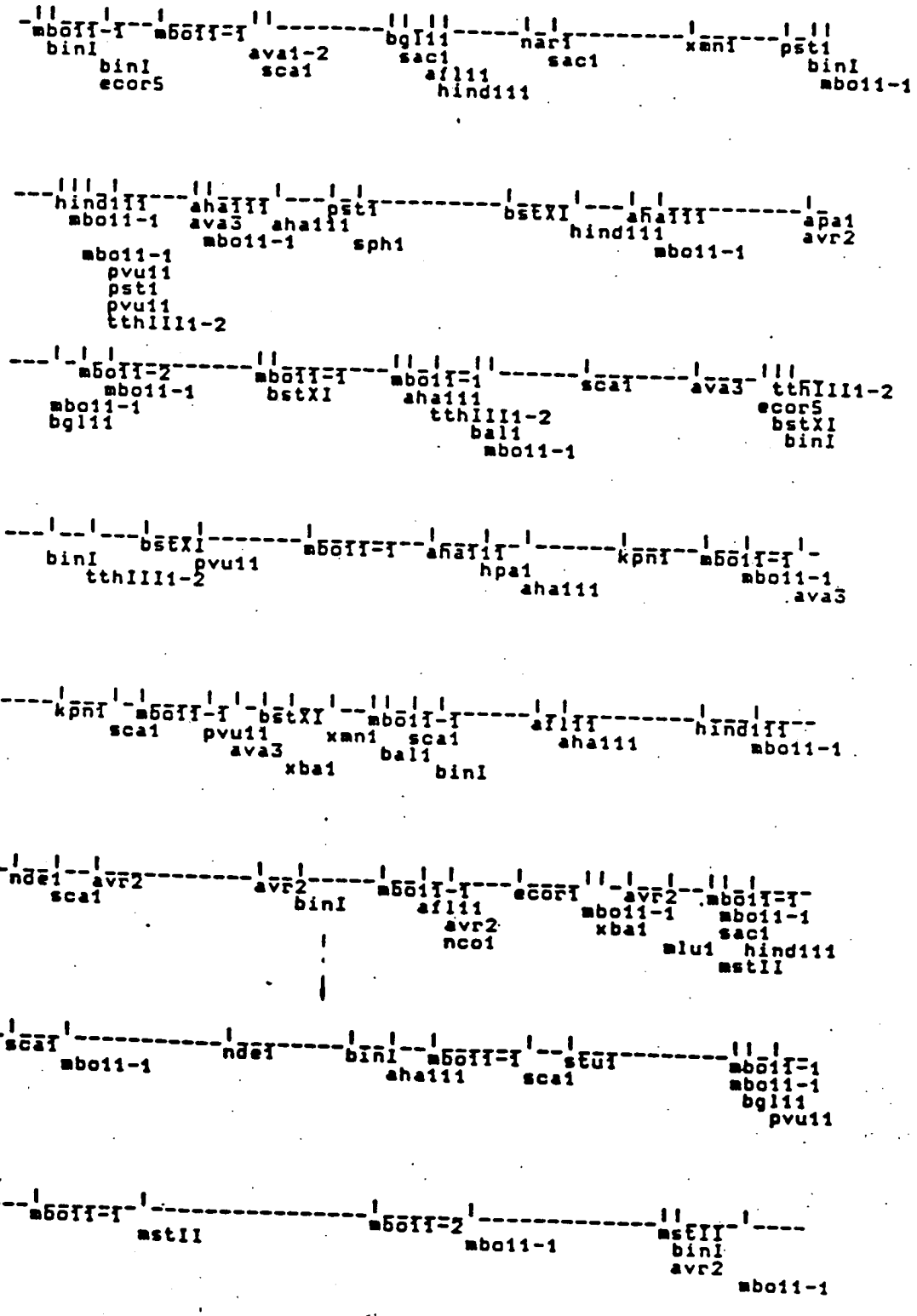
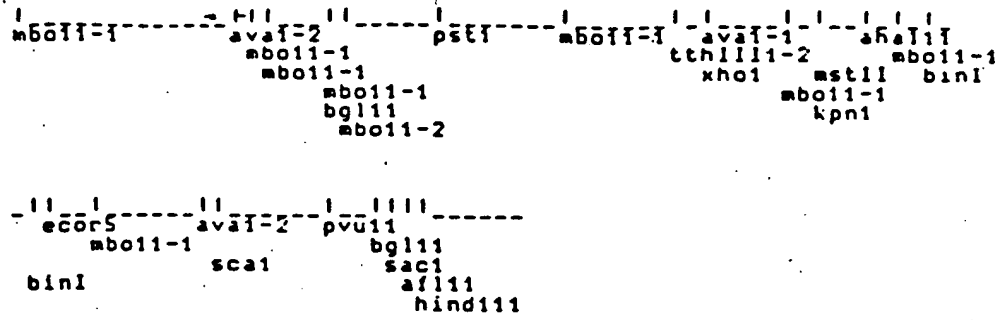



Figure 4
Page 2 of 12

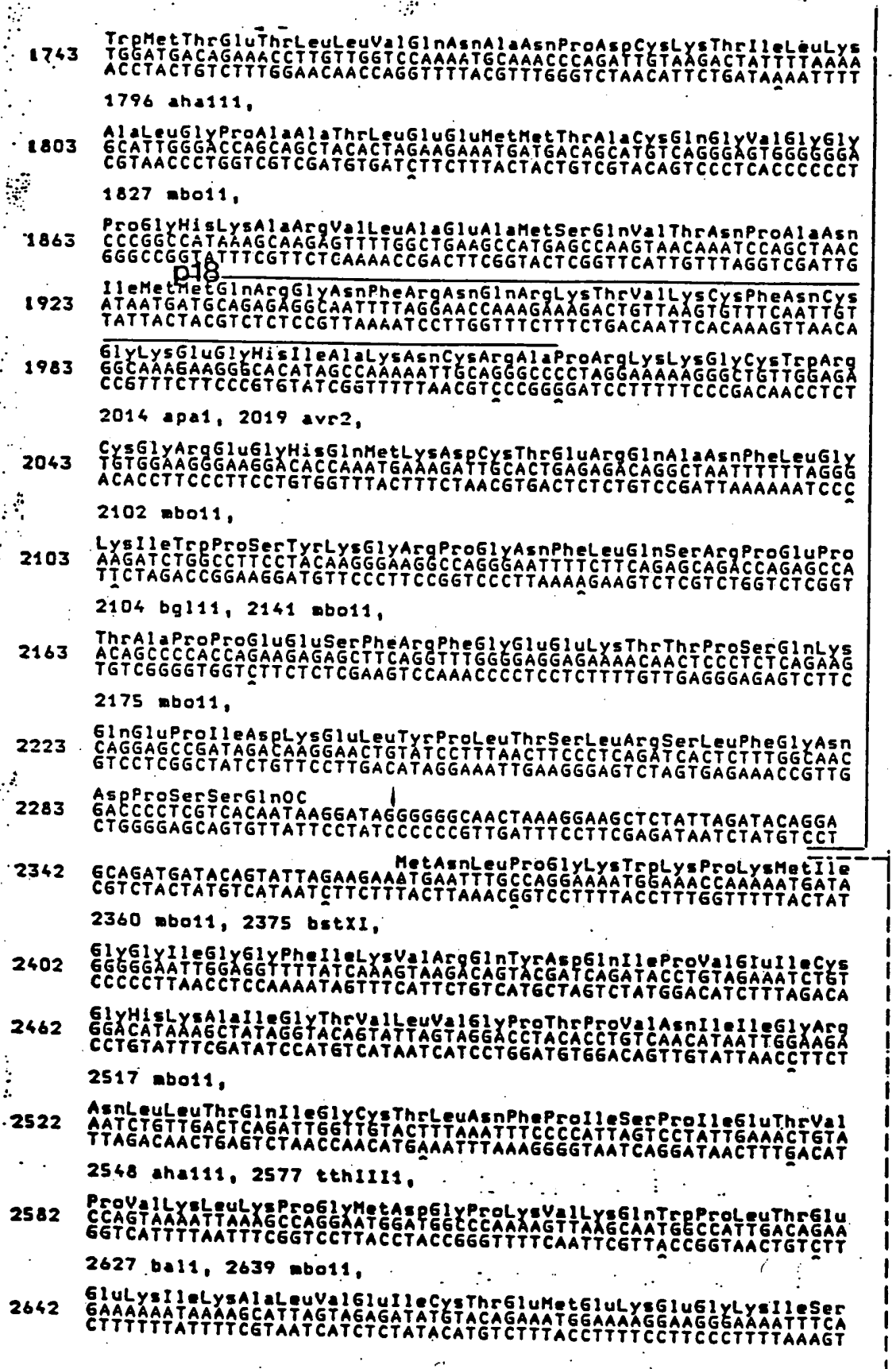



```
   1  CTGGAAGGGCTAATTTGGTCCCAAAGAAGACAAGAGATCCTTGATCTGTGGATCTACCACAC
      GACCTTCCCGATTAAACCAGGGTTTCTTCTGTTCTCTAGGAACTAGACACCTAGATGGTGTG

      26 mbo11, 50 binI,

  63  ACAAGGCTACTTCCCTGATTGGCAGAATTACACACCAGGGCCAGGGATCAGATATCCACT
      TGTTCCGATGAAGGGACTAACCGTCTTAATGTGTGGTCCCGGTCCCTAGTCTATAGGTGA

      107 binI, 113 ecor5,

 123  GACCTTTGGATGGTGCTTCAAGCTAGTACCAGTTGAGCCAGAGAAGGTAGAAGAGGCCAA
      CTGGAAACCTACCACGAAGTTCGATCATGGTCAACTCGGTCTCTTCCATCTTCTCCGGTT

      172 mbo11,

 183  TGAAGGAGAGAACAACAGCTTGTTACACCCTATGAGCCTGCATGGGATGGAGGACGCGGA
      ACTTCCTCTCTTGTTGTCGAACAATGTGGGATACTCGGACGTACCCTACCTCCTGCGCCT

 243  GAAAGAAGTGTTAGTGTGGAGGTTTGACAGCAAACTAGCATTTCATCACATGGCCCGAGA
      CTTTCTTCACAATCACACCTCCAAACTGTCGTTTGATCGTAAAGTAGTGTACCGGGCTCT

      296 aval,

 303  GCTGCATCCGGAGTACTACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCCGC
      CGACGTAGGCCTCATGATGTTTCTGACGACTGTAGCTCGAAAGATGTTCCCTGAAAGGCG

      314 sca1,

 363  TGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGTCCCTCAGATGC
      ACCCCTGAAAGGTCCCTCCGCACCGGACCCGCCCTGACCCCTCACCGCAGGGAGTCTACG

 423  TGCATATAAGCAGACTGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAG
      ACGTATATTCGTCTGACGAAAAACGGACATGACCCAGAGAGACCAATCTGGTCTAGACTC

      474 bgl11,

 483  CCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTT
      GGACCCTCGAGAGACCGATTGATCCCTTGGGTGACGAATTCGGAGTTATTTCGAACGGAA

      488 sac1, 518 afl11, 532 hind111,

 543  GAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCA
      CTCACGAAGTTCATCACACACGGGCAGACAACACACTGAGACCATTGATCTCTAGGGAGT

 603  GACCCTTTTAGTCAGTGTGGAAAAATCTCTAGCAGTGGCGCCCGAACAGGGACGCGAAAG
      CTGGGAAAATCAGTCACACCTTTTTAGAGATCGTCACCGCGGGCTTGTCCCTGCGCTTTC

      639 nar1,

 663  CGAAAGTAGAACCAGAGGAGCTCTCTCGACGCAGGACTCGGCTTGCTGAAGCGCGCACAG
      GCTTTCATCTTGGTCTCCTCGAGAGAGCTGCGTCCTGAGCCGAACGACTTCGCGCGTGTC

      680 sac1,

 723  CAAGAGGCGAGGGGCGGCGACTGGTGAGTACGCCAATTTTTGACTAGCGGAGGCTAGAAG
      GTTCTCCGCTCCCCGCCGCTGACCACTCATGCGGTTAAAAACTGATCGCCTCCGATCTTC

                MetGlyAlaArgAlaSerValLeuSerGlyGlyGluLeuAspLysTrpGlu  GAG
 783  GAGAGAGAGATGGGTGCGAGAGCGTCGGTATTAAGCGGGGGAGAATTAGATAAATGGGAA
      CTCTCTCTCTACCCACGCTCTCGCAGCCATAATTCGCCCCCTCTTAATCTATTTACCCTT
```

```
                LysIleArgLeuArgProGlyGlyLysLysLysTyrLysLeuLysHisIleValTrpAla
 843            AAAATTCGGTTAAGGCCAGGGGGAAAGAAAAAATATAAGTTAAAACATATAGTATGGGCA
                TTTTAAGCCAATTCCGGTCCCCCTTTCTTTTTTATATTCAATTTTGTATATCATACCCGT

                SerArgGluLeuGluArgPheAlaValAsnProGlyLeuLeuGluThrSerGluGlyCys
 903            AGCAGGGAGCTAGAACGATTCGCAGTCAATCCTGGCCTGTTAGAAACATCAGAAGGCTGC
                TCGTCCCTCGATCTTGCTAAGCGTCAGTTAGGACCGGACAATCTTTGTAGTCTTCCGACG

                959 pst1,

                ArgGlnIleLeuGlyGlnLeuGlnProSerLeuGlnThrGlySerGluGluLeuArgSer
 963            AGACAAATATTGGGACAGCTACAGCCATCCCTTCAGACAGGATCAGAAGAACTTAGATCA
                TCTGTTTATAACCCTGTCGATGTCGGTAGGGAAGTCTGTCCTAGTCTTCTTGAATCTAGT

                1002 binI, 1008 mbo11,

                LeuTyrAsnThrValAlaThrLeuTyrCysValHisGlnArgIleAspValLysAspThr
1023            TTATATAATACAGTAGCAACCCTCTATTGTGTACATCAAAGGATAGATGTAAAAGACACC
                AATATATTATGTCATCGTTGGGAGATAACACATGTAGTTTCCTATCTACATTTTCTGTGG

                LysGluAlaLeuGluLysIleGluGluGluGlnAsnLysSerLysLysLysAlaGlnGln
1083            AAGGAAGCTTTAGAGAAGATAGAGGAAGAGCAAAACAAAAGTAAGAAAAAGGCACAGCAA
                TTCCTTCGAAATCTCTTCTATCTCCTTCTCGTTTTGTTTTCATTCTTTTTCCGTGTCGTT

                1087 hind111, 1097 mbo11, 1107 mbo11,                    p25

                AlaAlaAlaAlaAlaGlyThrGlyAsnSerSerGlnValSerGlnAsnTyrProIleVal
1143            GCAGCAGCTGCAGCTGGTACAGGAAACAGCAGCCAGGTCAGCCAAAATTACCCTATAGTG
                CGTCGTCGACGTCGACCGTGTCCTTTGTCGTCGGTCCAGTCGGTTTTAATGGGATATCAC

                1147 pvu11, 1150 pst1, 1153 pvu11, 1156 tthIII1,

                GlnAsnLeuGlnGlyGlnMetValHisGlnAlaIleSerProArgThrLeuAsnAlaTrp
1203            CAGAACCTACAGGGGCAAATGGTACATCAGGCCATATCACCTAGAACTTTAAATGCATGG
                GTCTTGGATGTCCCCGTTTACCATGTAGTCCGGTATAGTGGATCTTGAAATTTACGTACC

                1250 aha111, 1255 ava3,

                ValLysValValGluGluLysAlaPheSerProGluValIleProMetPheSerAlaLeu
1263            GTAAAAGTAGTAGAAGAAAAGGCTTTCAGCCCAGAAGTAATACCCATGTTTTCAGCATTA
                CATTTTCATCATCTTCTTTTCCGAAAGTCGGGTCTTCATTATGGGTACAAAAGTCGTAAT

                1275 mbo11,

                SerGluGlyAlaThrProGlnAspLeuAsnThrMetLeuAsnThrValGlyGlyHisGln
1323            TCAGAAGGAGCCACCCCACAAGATTTAAACACCATGCTAAACACAGTGGGGGGACATCAA
                AGTCTTCCTCGGTGGGGTGTTCTAAATTTGTGGTACGATTTGTGTCACCCCCCTGTAGTT

                1346 aha111,

                AlaAlaMetGlnMetLeuLysGluThrIleAsnGluGluAlaAlaGluTrpAspArgVal
1383            GCAGCCATGCAAATGTTAAAAGAGACTATCAATGAGGAAGCTGCAGAATGGGATAGAGTG
                CGTCGGTACGTTTACAATTTTCTCTGATAGTTACTCCTTCGACGTCTTACCCTATCTCAC

                1423 pst1,

                HisProValHisAlaGlyProIleAlaProGlyGlnMetArgGluProArgGlySerAsp
1443            CATCCAGTGCATGCAGGGCCTATTGCACCAGGTCAAATGAGAGAACCAAGGGGAAGTGAC
                GTAGGTCACGTACGTCCCGGATAACGTGGTCCGGTTTACTCTCTTGGTTCCCCTTCACTG

                1451 sph1,

                IleAlaGlyThrThrSerThrLeuGlnGluGlnIleGlyTrpMetThrAsnAsnProPro
1503            ATAGCAGGAACTACTAGTACCCTTCAGGAACAAATAGGATGGATGACAAATAATCCACCT
                TATCGTCCTTGATGATCATGGGAAGTCCTTGTTTATCCTACCTACTGTTTATTAGGTGGA

                IleProValGlyGluIleTyrLysArgTrpIleIleLeuGlyLeuAsnLysIleValArg
1563            ATCCCAGTAGGAGAAATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAGTAAGA
                TAGGGTCATCCTCTTTAGATATTTTCTACCTATTAGGACCCTAATTTATTTTATCATTCT

                MetTyrSerProThrSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAsp
1623            ATGTATAGCCCTACCAGCATTCTGGACATAAGACAAGGACCAAAGGAACCCTTTAGAGAT
                TACATATCGGGATGGTCGTAAGACCTGTATTCTGTTCCTGGTTTCCTTGGGAAATCTCTA

                1636 bstXI,

                TyrValAspArgPheTyrLysThrLeuArgAlaGluGlnAlaSerGlnAspValLysAsn
1683            TATGTAGACCGGTTCTATAAAACTCTAAGAGCCGAACAAGCTTCACAGGATGTAAAAAAT
                ATACATCTGGCCAAGATATTTTGAGATTCTCGGCTTGTTCGAAGTGTCCTACATTTTTTA

                1720 hind111,
```

CONFIDENTIAL

Figure 4
Page 4 of 12



CONFIDENTIAL

Figure 4
Page 5 of 1:

```
                LysIleGlyProGluAsnProTyrAsnThrProValPheAlaIleLysLysLysAspSer
2702            AAAATTGGGCCTGAAAATCCATACAATACTCCAGTATTTGCTATAAAGAAAAAAGACAGT
                TTTTAACCCGGACTTTTAGGTATGTTATGAGGTCATAAACGATATTTCTTTTTTCTGTCA

                2759 sca1,

                ThrLysTrpArgLysLeuValAspPheArgGluLeuAsnLysArgThrGlnAspPheTrp
2762            ACTAAATGGAGAAAACTAGTAGATTTCAGAGAACTTAATAAAAGAACTCAAGACTTCTGG
                TGATTTACCTCTTTTGATCATCTAAAGTCTCTTGAATTATTTTCTTGAGTTCTGAAGACC

                GluValGlnLeuGlyIleProHisProGlnGlyOC
2822            GAAGTTCAGTTAGGAATACCACACCCGCAGGGTTAAAAAAAAGAAAAAATCAGTAACAGTA
                CTTCAAGTCAATCCTTATGGTGTGGGCGTCCCAATTTTTTTCTTTTTTAGTCATTGTCAT

                TTGGATGTGGGTGATGCATACTTTTCAGTTCCCTTAGATAAAGACTTTAGAAAGTATACTG
2882            AACCTACACCCACTACGTATGAAAAGTCAAGGGAATCTATTTCTGAAATCTTTCATATGAC

                2895 ava3,

                                                MetArgHisGlnGlyLeuAspIleSerThrMetTrp
2943            CATTTACCATACCTAGTATAAACAATGAGACACCAGGGATTAGATATCAGTACAATGTGG
                GTAAATGGTATGGATCATATTTGTTACTCTGTGGTCCCTAATCTATAGTCATGTTACACC

                2985 ecor5,

                LeuProGlnGlyTrpLysGlySerProAlaIlePheGlnSerSerMetThrLysIleLeu
3003            CTGCCACAGGGATGGAAAGGATCACCAGCAATATTCCAAAGTAGCATGACAAAAATCTTA
                GACGGTGTCCCTACCTTTCCTAGTGGTCGTTATAAGGTTTCATCGTACTGTTTTTAGAAT

                3003 tthIII1, 3006 bstXI, 3021 binI,

                GluProPheArgLysGlnAsnProAspIleValIleTyrGlnTyrMetAspAspLeuTyr
3063            GAGCCTTTTAGAAAACAGAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTAT
                CTCGGAAAATCTTTTGTCTTAGGTCTGTATCAATAGATAGTTATGTACCTACTAAACATA

                ValGlySerAspLeuGluIleGlyGlnHisArgThrLysIleGluGluLeuArgGlnHis
3123            GTAGGATCTGACTTAGAAATAGGGCAGCATAGAACAAAAATAGAGGAACTGAGACAGCAT
                CATCCTAGACTGAATCTTTATCCCGTCGTATCTTGTTTTTATCTCCTTGACTCTGTCGTA

                3126 binI, 3171 tthIII1,

                LeuLeuArgTrpGlyPheThrThrProAspLysLysHisGlnLysGluProProPheLeu
3183            CTGTTGAGGTGGGGATTTACCACACCAGACAAAAAACATCAGAAAGAACCTCCATTCCTT
                GACAACTCCACCCCTAAATGGTGTGGTCTGTTTTTTGTAGTCTTTCTTGGAGGTAAGGAA

                3234 bstXI,

                TrpMetGlyTyrGluLeuHisProAspLysTrpThrValGlnProIleMetLeuProGlu
3243            TGGATGGGTTATGAACTCCATCCTGATAAATGGACAGTACAGCCTATAATGCTGCCAGAA
                ACCTACCCAATACTTGAGGTAGGACTATTTACCTGTCATGTCGGATATTACGACGGTCTT

                LysAspSerTrpThrValAsnAspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSer
3303            AAAGACAGCTGGACTGTCAATGACATACAGAAGTTAGTGGGAAAATTGAATTGGGCAAGT
                TTTCTGTCGACCTGACAGTTACTGTATGTCTTCAATCACCCTTTTAACTTAACCCGTTCA

                3308 pvu11,

                GlnIleTyrAlaGlyIleLysValLysGlnLeuCysLysLeuLeuArgGlyThrLysAla
3363            CAGATTTATGCAGGGATTAAAGTAAAGCAGTTATGTAAACTCCTTAGAGGAACCAAAGCA
                GTCTAAATACGTCCCTAATTTCATTTCGTCAATACATTTGAGGAATCTCCTTGGTTTCGT

                LeuThrGluValIleProLeuThrGluGluAlaGluLeuGluLeuAlaGluAsnArgGlu
3423            CTAACAGAAGTAATACCACTAACAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGGGAG
                GATTGTCTTCATTATGGTGATTGTCTTCTTCGTCTCGATCTTGACCGTCTTTTGTCCCTC

                3447 mbo11,

                IleLeuLysGluProValHisGluValTyrTyrAspProSerLysAspLeuValAlaGlu
3483            ATTCTAAAAGAACCAGTACATGAAGTATATTATGACCCATCAAAAGACTTAGTAGCAGAA
                TAAGATTTTCTTGGTCATGTACTTCATATAATACTGGGTAGTTTTCTGAATCATCGTCTT

                IleGlnLysGlnGlyGlnGlyGlnTrpThrTyrGlnIleTyrGlnGluProPheLysAsn
3543            ATACAGAAGCAGGGGCAAGGCCAATGGACATATCAAATTTATCAAGAGCCATTTAAAAAT
                TATGTCTTCGTCCCCGTTCCGGTTACCTGTATAGTTTAAATAGTTCTCGGTAAATTTTTA

                3594 aha111,

                LeuLysThrGlyLysTyrAlaArgMetArgGlyAlaHisThrAsnAspValLysGlnLeu
3603            CTGAAAACAGGAAAGTATGCAAGGATGAGGGGTGCCCACACTAATGATGTAAAACAGTTA
                GACTTTTGTCCTTTCATACGTTCCTACTCCCCACGGGTGTGATTACTACATTTTGTCAAT

                3659 hpa1,
```

POL

CONFIDENTIAL



```
                ThrGluAlaValGlnLysValSe..hrGluSerIleValIleTrpGlyLysIl..roLys
3663            ACAGAGGCAGTGCAAAAAGTATCCACAGAAAGCATAGTAATATGGGGAAAGATTCCTAAA
                TGTCTCCGTCACGTTTTTCATAGGTGTCTTTCGTATCATTATACCCCTTTCTAAGGATTT

                PheLysLeuProIleGlnLysGluThrTrpGluAlaTrpTrpMetGluTyrTrpGlnAla
3723            TTTAAACTACCCATACAAAAGGAAACATGGGAAGCATGGTGGATGGAGTATTGGCAAGCT
                AAATTTGATGGGTATGTTTTCCTTTGTACCCTTCGTACCACCTACCTCATAACCGTTCGA

                3723 aha111,

                ThrTrpIleProGluTrpGluPheValAsnThrProProLeuValLysLeuTrpTyrGln
3783            ACCTGGATTCCTGAGTGGGAGTTTGTCAATACCCCTCCCTTAGTGAAATTATGGTACCAG
                TGGACCTAAGGACTCACCCTCAAACAGTTATGGGGAGGGAATCACTTTAATACCATGGTC

                3835 kpn1,

                LeuGluLysGluProIleValGlyAlaGluThrPheTyrValAspGlyAlaAlaAsnArg
3843            TTAGAGAAAGAACCCATAGTAGGAGCAGAAACTTTCTATGTAGATGGGGCAGCTAATAGG
                AATCTCTTTCTTGGGTATCATCCTCGTCTTTGAAAGATACATCTACCCCGTCGATTATCC

                GluThrLysLeuGlyLysAlaGlyTyrValThrAspArgGlyArgGlnLysValValSer
3903            GAGACTAAATTAGGAAAAGCAGGATATGTTACTGACAGAGGAAGACAAAAAGTTGTCTCC
                CTCTGATTTAATCCTTTTCGTCCTATACAATGACTGTCTCCTTCTGTTTTTCAACAGAGG

                3943 mbo11,

                IleAlaAspThrThrAsnGlnLysThrGluLeuGlnAlaIleHisLeuAlaLeuGlnAsp
3963            ATAGCTGACACAACAAATCAGAAGACTGAATTACAAGCAATTCATCTAGCTTTGCAGGAT
                TATCGACTGTGTTGTTTAGTCTTCTGACTTAATGTTCGTTAAGTAGATCGAAACGTCCTA

                3983 mbo11,

                SerGlyLeuGluValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAla
4023            TCGGGATTAGAAGTAAACATAGTAACAGACTCACAATATGCATTAGGAATCATTCAAGCA
                AGCCCTAATCTTCATTTGTATCATTGTCTGAGTGTTATACGTAATCCTTAGTAAGTTCGT

                4060 ava3,

                GlnProAspLysSerGluSerGluLeuValSerGlnIleIleGluGlnLeuIleLysLys
4083            CAACCAGATAAGAGTGAATCAGAGTTAGTCAGTCAAATAATAGAGCAGTTAATAAAAAAG
                GTTGGTCTATTCTCACTTAGTCTCAATCAGTCAGTTTATTATCTCGTCAATTATTTTTTC

                GluLysValTyrLeuAlaTrpValProAlaHisLysGlyIleGlyGlyAsnGluGlnVal
4143            GAAAAGGTCTACCTGGCATGGGTACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTA
                CTTTTCCAGATGGACCGTACCCATGGTCGTGTGTTTCCTTAACCTCCTTTACTTGTTCAT

                4163 kpn1,

                AspLysLeuValSerAlaGlyIleArgLysValLeuPheLeuAsnGlyIleAspLysAla
4203            GATAAATTAGTCAGTGCTGGAATCAGGAAAGTACTATTTTTGAATGGAATAGATAAGGCC
                CTATTTAATCAGTCACGACCTTAGTCCTTTCATGATAAAAACTTACCTTATCTATTCCGG

                4232 sca1,

                GlnGluGluHisGluLysTyrHisSerAsnTrpArgAlaMetAlaSerAspPheAsnLeu
4263            CAAGAAGAACATGAGAAATATCACAGTAATTGGAGAGCAATGGCTAGTGATTTTAACCTG
                GTTCTTCTTGTACTCTTTATAGTGTCATTAACCTCTCGTTACCGATCACTAAAATTGGAC

                4266 mbo11,

                ProProValValAlaLysGluIleValAlaSerCysAspLysCysGlnLeuLysGlyGlu
4323            CCACCTGTAGTAGCAAAAGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAA
                GGTGGACATCATCGTTTTCTTTATCATCGGTCGACACTATTTACAGTCGATTTTCCTCTT

                4352 pvu11,

                AlaMetHisGlyGlnValAspCysSerProGlyIleTrpGlnLeuAspCysThrHisLeu
4383            GCCATGCATGGACAAGTAGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACATCTA
                CGGTACGTACCTGTTCATCTGACATCAGGTCCTTATACCGTTGATCTAACATGTGTAGAT

                4386 ava3, 4410 bstXI, 4439 xba1,

                GluGlyLysIleIleLeuValAlaValHisValAlaSerGlyTyrIleGluAlaGluVal
4443            GAAGGAAAAATTATCCTGGTAGCAGTTCATGTAGCCAGTGGATATATAGAAGCAGAAGTT
                CTTCCTTTTTAATAGGACCATCGTCAAGTACATCGGTCACCTATATATCTTCGTCTTCAA

                4497 xmn1,

                IleProAlaGluThrGlyGlnGluThrAlaTyrPheLeuLeuLysLeuAlaGlyArgTrp
4503            ATTCCAGCAGAGACAGGGCAGGAAACAGCATATTTTCTCTTAAAATTAGCAGGAAGATGG
                TAAGGTCGTCTCTGTCCCGTCCTTTGTCGTATAAAAGAGAATTTTAATCGTCCTTCTACC

                4555 mbo11, 4560 ba11,
```

CONFIDENTIAL



```
                ProValLysThrIleHisThrAspAsnGlySerAsnPheThrSerThrThrValLysAla
4563            CCAGTAAAAACAATACATACAGACAATGGCAGCAATTTCACCAGTACTACGGTTAAGGCC
                GGTCATTTTTGTTATGTATGTCTGTTACCGTCGTTAAAGTGGTCATGATGCCAATTCCGG

                4605 sca1,

                AlaCysTrpTrpAlaGlyIleLysGlnGluPheGlyIleProTyrAsnProGlnSerGln
4623            GCCTGTTGGTGGGCAGGGATCAAGCAGGAATTTGGCATTCCCTACAATCCCCAAAGTCAA
                CGGACAACCACCCGTCCCTAGTTCGTCCTTAAACCGTAAGGGATGTTAGGGGTTTCAGTT

                4639 binI,

                GlyValValGluSerMetAsnAsnGluLeuLysLysIleIleGlyGlnValArgAspGln
4683            GGAGTAGTAGAATCTATGAATAATGAATTAAAGAAAATTATAGGACAGGTAAGAGATCAG
                CCTCATCATCTTAGATACTTATTACTTAATTTCTTTTAATATCCTGTCCATTCTCTAGTC

                AlaGluHisLeuLysThrAlaValGlnMetAlaValPheIleHisAsnPheLysArgLys
4743            GCTGAACACCTTAAGACAGCAGTACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAA
                CGACTTGTGGAATTCTGTCGTCATGTTTACCGTCATAAGTAGGTGTTAAAATTTTCTTTT

                4752 af111, 4791 aha111,

                GlyGlyIleGlyGlyTyrSerAlaGlyGluArgIleValAspIleIleAlaThrAspIle
4803            GGGGGGATTGGGGGATACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATA
                CCCCCCTAACCCCCTATGTCACGTCCCCTTTCTTATCATCTGTATTATCGTTGTCTGTAT

                GlnThrLysGluLeuGlnLysGlnIleThrLysIleGlnAsnPheArgValTyrTyrArg
4863            CAAACTAAAGAACTACAAAAGCAAATTACAAAAATTCAAAATTTTCGGGTTTATTACAGG
                GTTTGATTTCTTGATGTTTTCGTTTAATGTTTTTAAGTTTTAAAAGCCCAAATAATGTCC

                AspAsnLysAspProLeuTrpLysGlyProAlaLysLeuLeuTrpLysGlyGluGlyAla
4923            GACAACAAAGATCCCCTTTGGAAAGGACCAGCAAAGCTTCTCTGGAAAGGTGAAGGGGCA
                CTGTTGTTTCTAGGGGAAACCTTTCCTGGTCGTTTCGAAGAGACCTTTCCACTTCCCCGT

                4956 hind111,

                ValValIleGlnAspAsnSerAspIleLysValValProArgArgLysAlaLysIleIle
4983            GTAGTAATACAAGATAATAGTGACATAAAAGTAGTGCCAAGAAGAAAAGCAAAAATCATT
                CATCATTATGTTCTATTATCACTGTATTTTCATCACGGTTCTTCTTTTCGTTTTTAGTAA

                5023 mbo11,

                      MetGluAsnArgTrpGlnValMetIleValTrpGlnValAspArgMetArgIle
ArgAspTyrGlyLysGlnMetAlaGlyAspAspCysValAlaSerArgGlnAspGluAsp
5043            AGGGATTATGGAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGAT
                TCCCTAATACCTTTTGTCTACCGTCCACTACTAACACACCGTTCATCTGTCCTACTCCTA

                ArgTrpTrpLysSerLeuValLysHisHisMetTyrIleSerLysLysAlaLysGlyTrp
AM
5103            TAGAACATGGAAAAGTTTAGTAAAACACCATATGTATATTTCAAAGAAAGCTAAAGGATGG
                ATCTTGTACCTTTTCAAATCATTTTGTGGTATACATATAAAGTTTCTTTCGATTTCCTACC

                5131 nde1,

                   PheTyrArgHisHisTyrGluSerThrHisProArgValSerSerGluValHisIle
5163               TTTTATAGACATCACTATGAAAGTACTCATCCAAGAGTAAGTTCAGAAGTACACATC
                   AAAATATCTGTAGTGATACTTTCATGAGTAGGTTCTCATTCAAGTCTTCATGTGTAG

                5185 sca1,

                ProLeuGlyAspAlaLysLeuValIleThrThrTyrTrpGlyLeuHisThrGlyGluArg
5221            CCCCTAGGGGATGCTAAATTGGTAATAACAACATATTGGGGTCTGCATACAGGAGAAAGA
                GGGGATCCCCTACGATTTAACCATTATTGTTGTATAACCCCAGACGTATGTCCTCTTTCT

                5223 avr2,

                GluTrpHisLeuGlyGlnGlyValAlaIleGluTrpArgLysLysLysTyrSerThrGln
5281            GAATGGCATTTGGGTCAGGGAGTCGCCATAGAATGGAGGAAAAAGAAATATAGCACACAA
                CTTACCGTAAACCCGGTCCCTCAGCGGTATCTTACCTCCTTTTTCTTTATATCGTGTGTT

                ValAspProGlyLeuAlaAspGlnLeuIleHisLeuHisTyrPheAspCysPheSerGlu
5341            GTAGACCCTGGCCTAGCAGACCAACTAATTCATCTGCATTATTTTGATTGTTTTCAGAA
                CATCTGGGACCGGATCGTCTGGTTGATTAAGTAGACGTAATAAAACTAACAAAAAGTCTT

                SerAlaIleLysAsnAlaIleLeuGlyTyrArgValSerProArgCysGluTyrGlnAla
5401            TCTGCTATAAAAAATGCCATATTAGGATATAGAGTTAGTCCTAGGTGTGAATATCAAGCA
                AGACGATATTTTTTACGGTATAATCCTATATCTCAATCAGGATCCACACTTATAGTTCGT

                5440 avr2,

                GlyHisAsnLysValGlySerLeuGlnTyrLeuAlaLeuAlaAlaLeuIleThrProLys
5461            GGACATAACAAGGTAGGATCTCTACAATACTTGGCACTAGCAGCATTAATAACACCAAAA
                CCTGTATTGTTCCATCCTAGAGATGTTATGAACCGTGATCGTCGTAATTATTGTGGTTTT

                5476 binI,
```

CONFIDENTIAL



```
                LysThrLysProProLeuProSerValLysLysLeuThrGluAspArgTrpAsnLysPro
5521            AAGACAAAGCCACCTTTGCCTAGTGTTAAGAAACTGACAGAGGATAGATGGAACAAGCCC
                TTCTGTTTCGGTGGAAACGGATCACAATTCTTTGACTGTCTCCTATCTACCTTGTTCGGG

                GlnLysThrLysGlyHisArgGlySerHisThrMetAsnGlyHisAM
5581            CAGAAGACCAAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAGAGCTTTTAGAGG
                GTCTTCTGGTTCCCGGTGTCTCCCTCGGTATGTTACTTACCTGTGATCTCGAAAATCTCC

                5583 mbo11,

5641            AGCTTAAGAGAGAAGCTGTTAGACATTTTCCTAGGCCATGGCTCCATAGCTTAGGACAAT
                TCGAATTCTCTCTTCGACAATCTGTAAAAGGATCCGGTACCGAGGTATCGAATCCTGTTA

                5643 af111, 5670 avr2, 5676 nco1,

5701            ATATCTATGAAACTTATGGGGATACTTGGGCAGGAGTGGAAGCCATAATAAGAATTCTGC
                TATAGATACTTTGAATACCCCTATGAACCCGTCCTCACCTTCGGTATTATTCTTAAGACG

                5752 ecor1,

5761            AACAACTGCTGTTTATTCATTTCAGAATTGGGTGTCAACATAGCAGAATAGGCATTATTC
                TTGTTGACGACAAATAAGTAAAGTCTTAACCCACAGTTGTATCGTCTTATCCGTAATAAG

5821            AACAGAGGAGAGCAAGAAGAAATGGAGCCAGTAGATCCTAATCTAGAGCCCTGGAAGCAT
                TTGTCTCCTCTCGTTCTTCTTTACCTCGGTCATCTAGGATTAGATCTCGGGACCTTCGTA

                5836 mbo11, 5862 xba1,

5881            CCAGGAAGTCAGCCTAGGACTGCTTGTAACAATTGCTATTGTAAAAAGTGTTGCTTTCAT
                GGTCCTTCAGTCGGATCCTGACGAACATTGTTAACGATAACATTTTTCACAACGAAAGTA

                5893 avr2,

5941            TGCTACGCGTGTTTCACAAGAAAAGGCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGA
                ACGATGCGCACAAAGTGTTCTTTTCCGAATCCGTAGAGGATACCGTCCTTCTTCGCCTCT

                5945 mlu1, 5988 mbo11,

6001            CAGCGACGAAGAGCTCCTCAGGACAGTCAGACTCATCAAGCTTCTCTATCAAAGCAGTAA
                GTCGCTGCTTCTCGAGGAGTCCTGTCAGTCTGAGTAGTTCGAAGAGATAGTTTCGTCATT

                6008 mbo11, 6011 sac1, 6016 mstII, 6038 hind111,

6061            GTAGTAAATGTAATGCAATCTTTACAAATATTAGCAATAGTATCATTAGTAGTAGTAGCA
                CATCATTTACATTACGTTAGAAATGTTTATAATCGTTATCATAGTAATCATCATCATCGT

6121            ATAATAGCAATAGTTGTGTGGACCATAGTACTCATAGAATATAGGAAAATATTAAGACAA
                TATTATCGTTATCAACACACCTGGTATCATGAGTATCTTATATCCTTTTATAATTCTGTT

                6147 sca1,

6181            AGAAAATAGACAGATTAATTGATAGAATAAGAGAAAAAGCAGAAGACAGTGGCAATGAAA  MetLys  ENV
                TCTTTTATCTGTCTAATTAACTATCTTATTCTCTTTTTCGTCTTCTGTCACCGTTACTTT

                6222 mbo11,

6241            ValLysGlyThrArgArgAsnTyrGlnHisLeuTrpArgTrpGlyThrLeuLeuLeuGly
                GTGAAGGGGACCAGGAGGAATTATCAGCACTTGTGGAGATGGGGCACCTTGCTCCTTGGG
                CACTTCCCCTGGTCCTCCTTAATAGTCGTGAACACCTCTACCCCGTGGAACGAGGAACCC

6301            MetLeuMetIleCysSerAlaThrGluLysLeuTrpValThrValTyrTyrGlyValPro
                ATGTTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTCACAGTTTATTATGGAGTACCT
                TACAACTACTAGACATCACGATGTCTTTTTAACACCCAGTGTCAAATAATACCTCATGGA

6361            ValTrpLysGluAlaThrThrThrLeuPheCysAlaSerAspAlaArgAlaTyrAspThr
                GTGTGGAAAGAAGCAACTACCACTCTATTTTGTGCATCAGATGCTAGAGCATATGATACA
                CACACCTTTCTTCGTTGATGGTGAGATAAAACACGTAGTCTACGATCTCGTATACTATGT

                6410 nde1,

6421            GluValHisAsnValTrpAlaThrHisAlaCysValProThrAspProAsnProGlnGlu
                GAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAACCCACAAGAA
                CTCCATGTATTACAAACCCGGTGTGTACGGACACATGGGTGTCTGGGGTTGGGTGTTCTT

6481            ValValLeuGlyAsnValThrGluAshPheAsnMetTrpLysAsnAsnMetValGluGln
                GTAGTATTGGGAAATGTGACAGAAAATTTTAACATGTGGAAAAATAACATGGTAGAACAG
                CATCATAACCCTTTACACTGTCTTTTAAAATTGTACACCTTTTTATTGTACCATCTTGTC

6541            MetGlnGluAspIleIleSerLeuTrpAspGlnSerLeuLysProCysValLysLeuThr
                ATGCAGGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGTGTAAAATTAACC
                TACGTCCTCCTATATTAGTCAAATACCCTAGTTTCGGATTTCGGTACACATTTTAATTGG

                6567 bin1,
```

CONFIDENTIAL



```
                ProLeuCysValThrLeuAsnCysThrAspLeuGlyLysAlaThrAsnThrAsnSerSer
5601            CCACTCTGTGTTACTTTAAATTGCACTGATTTGGGGAAGGCTACTAATACCAATAGTAGT
                GGTGAGACACAATGAAATTTAACGTGACTAAACCCCTTCCGATGATTATGGTTATCATCA

                6615 aha111,

                AsnTrpLysGluGluIleLysGlyGluIleLysAsnCysSerPheAsnIleThrThrSer
5661            AATTGGAAAGAAGAAATAAAAGGAGAAATAAAAAACTGCTCTTTCAATATCACCACAAGC
                TTAACCTTTCTTCTTTATTTTCCTCTTTATTTTTTGACGAGAAAGTTATAGTGGTGTTCG

                6670 mbo11,

                IleArgAspLysIleGlnLysGluAsnAlaLeuPheArgAsnLeuAspValValProIle
5721            ATAAGAGATAAGATTCAGAAAGAAAATGCACTTTTTCGTAACCTTGATGTAGTACCAATA
                TATTCTCTATTCTAAGTCTTTCTTTTACGTGAAAAAGCATTGGAACTACATCATGGTTAT

                AspAsnAlaSerThrThrThrAsnTyrThrAsnTyrArgLeuIleHisCysAsnArgSer
5781            GATAATGCTAGTACTACTACCAACTATACCAACTATAGGTTGATACATTGTAACAGATCA
                CTATTACGATCATGATGATGGTTGATATGGTTGATATCCAACTATGTAACATTGTCTAGT

                6790 sca1,

                ValIleThrGlnAlaCysProLysValSerPheGluProIleProIleHisTyrCysThr
5841            GTCATTACACAGGCCTGTCCAAAGGTATCATTTGAGCCAATTCCCATACATTATTGTACC
                CAGTAATGTGTCCGGACAGGTTTCCATAGTAAACTCGGTTAAGGGTATGTAATAACATGG

                6851 stu1,

                ProAlaGlyPheAlaIleLeuLysCysAsnAsnLysThrPheAsnGlyLysGlyProCys
5901            CCGGCTGGTTTTGCGATTCTAAAGTGTAATAATAAAACGTTCAATGGAAAAGGACCATGT
                GGCCGACCAAAACGCTAAGATTTCACATTATTATTTTGCAAGTTACCTTTTCCTGGTACA

                ThrAsnValSerThrValGlnCysThrHisGlyIleArgProIleValSerThrGlnLeu
5961            ACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAATAGTGTCAACTCAACTG
                TGTTTACAGTCGTGTCATGTTACATGTGTACCTTAATCCGGTTATCACAGTTGAGTTGAC

                LeuLeuAsnGlySerLeuAlaGluGluGluValValIleArgSerAspAsnPheThrAsn
7021            CTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTTCACGAAC
                GACAATTTACCGTCAGATCGTCTTCTTCTCCATCATTAATCTAGACTGTTAAAGTGCTTG

                7042 mbo11, 7045 mbo11, 7060 bgl11,

                AsnAlaLysThrIleIleValGlnLeuAsnGluSerValAlaIleAsnCysThrArgPro
7081            AATGCTAAAACCATAATAGTACAGCTGAATGAATCTGTAGCAATTAACTGTACAAGACCC
                TTACGATTTTGGTATTATCATGTCGACTTACTTAGACATCGTTAATTGACATGTTCTGGG

                7102 pvu11,

                AsnAsnAsnThrArgLysSerIleTyrIleGlyProGlyArgAlaPheHisThrThrGly
7141            AACAACAATACAAGAAAAAGTATCTATATAGGACCAGGGAGAGCATTTCATACAACAGGA
                TTGTTGTTATGTTCTTTTTCATAGATATATCCTGGTCCCTCTCGTAAAGTATGTTGTCCT

                7199 mbo11,

                ArgIleIleGlyAspIleArgLysAlaHisCysAsnIleSerArgAlaGlnTrpAsnAsn
7201            AGAATAATAGGAGATATAAGAAAAGCACATTGTAACATTAGTAGAGCACAATGGAATAAC
                TCTTATTATCCTCTATATTCTTTTCGTGTAACATTGTAATCATCTCGTGTTACCTTATTG

                ThrLeuGluGlnIleValLysLysLeuArgGluGlnPheGlyAsnAsnLysThrIleVal
7261            ACTTTAGAACAGATAGTTAAAAAATTAAGAGAACAGTTTGGGAATAATAAAACAATAGTC
                TGAAATCTTGTCTATCAATTTTTTAATTCTCTTGTCAAACCCTTATTATTTTGTTATCAG

                PheAsnGlnSerSerGlyGlyAspProGluIleValMetHisSerPheAsnCysArgGly
7321            TTTAATCAATCCTCAGGAGGGGACCCAGAAATTGTAATGCACAGTTTTAATTGTAGAGGG
                AAATTAGTTAGGAGTCCTCCCCTGGGTCTTTAACATTACGTGTCAAAATTAACATCTCCC

                7331 mstII,

                GluPhePheTyrCysAsnThrThrGlnLeuPheAsnAsnThrTrpArgLeuAsnHisThr
7381            GAATTTTTCTACTGTAATACAACACAACTGTTTAATAATACATGGAGGTTAAATCACACT
                CTTAAAAAGATGACATTATGTTGTGTTGACAAATTATTATGTACCTCCAATTTAGTGTGA

                GluGlyThrLysGlyAsnAspThrIleIleLeuProCysArgIleLysGlnIleIleAsn
7441            GAAGGAACTAAAGGAAATGACACAATCATACTCCCATGTAGAATAAAACAAATTATAAAC
                CTTCCTTGATTTCCTTTACTGTGTTAGTATGAGGGTACATCTTATTTTGTTTAATATTTG

                MetTrpGlnGluValGlyLysAlaMetTyrAlaProProIleGlyGlyGlnIleSerCys
7501            ATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCCTCCCATTGGAGGACAAATTAGTTGT
                TACACCGTCCTTCATCCTTTTCGTTACATACGGGGAGGGTAACCTCCTGTTTAATCAACA

                SerSerAsnIleThrGlyLeuLeuLeuThrArgAspGlyGlyThrAsnValThrAsnAsp
7561            TCATCAAATATTACAGGGCTGCTATTAACAAGAGATGGTGGTACAAATGTAACTAATGAC
                AGTAGTTTATAATGTCCCGACGATAATTGTTCTCTACCACCATGTTTACATTGATTACTG
```

CONFIDENTIAL



```
                ThrGluValPheArgProGlyGlyGlyAspMetArgAspAsnTrpArgSerGluLeuTyr
7621            ACCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATAT
                TGGCTCCAGAAGTCTGGACCTCCTCCTCTATACTCCCTGTTAACCTCTTCACTTAATATA

                7628 mbo11,

                LysTyrLysValIleLysIleGluProLeuGlyIleAlaProThrLysAlaLysArgArg
7681            AAATATAAAGTAATAAAAATTGAACCATTAGGAATAGCACCCACCAAGGCAAAGAGAAGA
                TTTATATTTCATTATTTTTAACTTGGTAATCCTTATCGTGGGTGGTTCCGTTTCTCTTCT

                7736 mbo11,

                ValValGlnArgGluLysArgAlaValGlyIleValGlyAlaMetPheLeuGlyPheLeu
7741            GTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAGTAGGAGCTATGTTCCTTGGGTTCTTG
                CACCACGTCTCTCTTTTTTCTCGTCACCCTTATCATCCTCGATACAAGGAACCCAAGAAC

                GlyAlaAlaGlySerThrMetGlyAlaValSerLeuThrLeuThrValGlnAlaArgGln
7801            GGAGCAGCAGGAAGCACTATGGGCGCAGTGTCATTGACGCTGACGGTACAGGCCAGACAA
                CCTCGTCGTCCTTCGTGATACCCGCGTCACAGTAACTGCGACTGCCATGTCCGGTCTGTT

                LeuLeuSerGlyIleValGlnGlnGlnAsnAsnLeuLeuArgAlaIleGluAlaGlnGln
7861            TTATTGTCTGGTATAGTGCAACAGCAGAACAATTTGCTGAGGGCTATTGAGGCGCAACAA
                AATAACAGACCATATCACGTTGTCGTCTTGTTAAACGACTCCCGATAACTCCGCGTTGTT

                HisLeuLeuGlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgValLeuAlaVal
7921            CATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTCCAGGCAAGAGTCCTGGCTGTG
                GTAGACAACGTTGAGTGTCAGACCCCGTAGTTCGTCGAGGTCCGTTCTCAGGACCGACAC

                GluArgTyrLeuArgAspGlnGlnLeuLeuGlyIleTrpGlyCysSerGlyLysLeuIle
7981            GAAAGATACCTAAGGGATCAACAGCTCCTAGGGATTTGGGGTTGCTCTGGAAAACTCATT
                CTTTCTATGGATTCCCTAGTTGTCGAGGATCCCTAAACCCCAACGAGACCTTTTGAGTAA

                7989 mstII, 7995 binI, 8007 avr2,

                CysThrThrAlaValProTrpAsnAlaSerTrpSerAsnLysSerLeuGluAspIleTrp
8041            TGCACCACTGCTGTGCCTTGGAATGCTAGTTGGAGTAATAAATCTCTGGAAGACATTTGG
                ACGTGGTGACGACACGGAACCTTACGATCAACCTCATTATTTAGAGACCTTCTGTAAACC

                8089 mbo11,

                AspAsnMetThrTrpMetGlnTrpGluArgGluIleAspAsnTyrThrAsnThrIleTyr
8101            GATAACATGACCTGGATGCAGTGGGAAAGAGAAATTGACAATTACACAAACACAATATAC
                CTATTGTACTGGACCTACGTCACCCTTTCTCTTTAACTGTTAATGTGTTTGTGTTATATG

                ThrLeuLeuGluGluSerGlnAsnGlnGlnGluLysAsnGluGlnGluLeuLeuGluLeu
8161            ACCTTACTTGAAGAATCGCAGAACCAACAAGAAAAGAATGAACAAGAATTATTAGAATTG
                TGGAATGAACTTCTTAGCGTCTTGGTTGTTCTTTTCTTACTTGTTCTTAATAATCTTAAC

                8170 mbo11,

                AspLysTrpAlaSerLeuTrpAsnTrpPheSerIleThrAsnTrpLeuTrpTyrIleLys
8221            GATAAGTGGGCAAGTTTGTGGAATTGGTTTAGCATAACAAACTGGCTGTGGTATATAAAG
                CTATTCACCCGTTCAAACACCTTAACCAAATCGTATTGTTTGACCGACACCATATATTTC

                IlePheIleMetIleValGlyGlyLeuValGlyLeuArgIleValPheAlaValLeuSer
8281            ATATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTGCTTTCT
                TATAAGTATTACTATCATCCTCCGAACCATCCAAATTCTTATCAAAAACGACACGAAAGA

                IleValAsnArgValArgGlnGlyTyrSerProLeuSerPheGlnThrArgLeuProVal
8341            ATAGTGAATAGAGTTAGGCAGGGATACTCACCATTGTCATTTCAGACCCGCCTCCCAGTC
                TATCACTTATCTCAATCCGTCCCTATGAGTGGTAACAGTAAAGTCTGGGCGGAGGGTCAG

                8400 ava1,

                ProArgGlyProAspArgProAspGlyIleGluGluGluGlyGlyGluArgAspArgAsp
8401            CCGAGGGGACCCGACAGGCCCGATGGAATCGAAGAAGAAGGTGGAGAGAGAGACAGAGAC
                GGCTCCCCTGGGCTGTCCGGGCTGCCTTAGCTTCTTCTTCCACCTCTCTCTCTGTCTCTG

                8431 mbo11, 8434 mbo11,

                ArgSerValArgLeuValAspGlyPheLeuAlaLeuIleTrpGluAspLeuArgSerLeu
8461            AGATCCGTTCGATTAGTGGATGGATTCTTAGCACTTATCTGGGAAGATCTGCGGAGCCTG
                TCTAGGCAAGCTAATCACCTACCTAAGAATCGTGAATAGACCCTTCTAGACGCCTCGGAC

                8503 mbo11, 8505 bglii,

                CysLeuPheSerTyrArgArgLeuArgAspLeuLeuLeuIleAlaAlaArgThrValGlu
8521            TGCCTCTTCAGCTACCGCCGCTTGAGAGACTTACTCTTGATTGCAGCGAGGACTGTGGAA
                ACGGAGAAGTCGATGGCGGCGAACTCTCTGAATGAGAACTAACGTCGCTCCTGACACCTT

                8525 mbo11,
```

CONFIDENTIAL

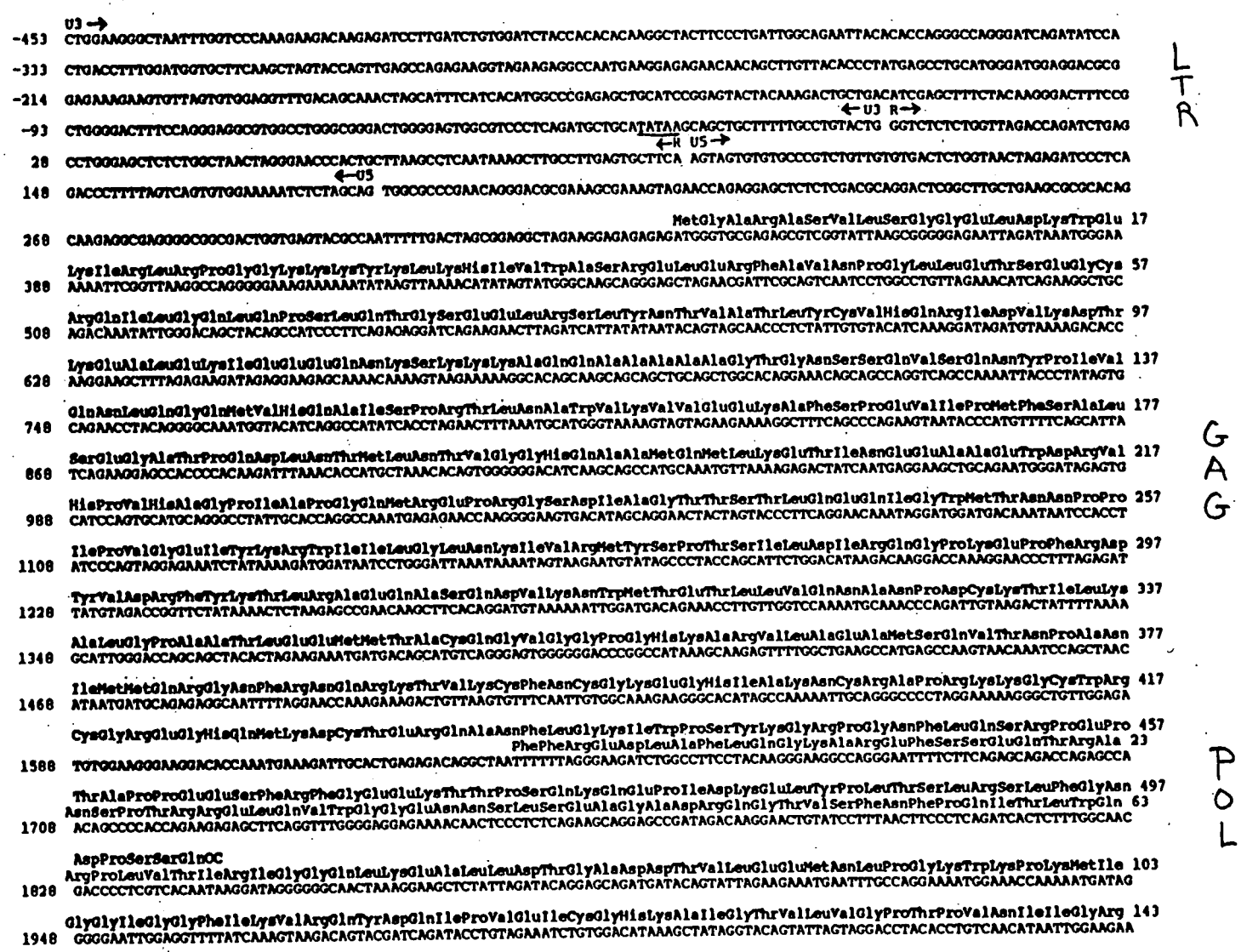


```
                IleLeuGlyHisArgGlyTrpG..AlaLeuLysTyrTrpTrpSerLeuLeu6.nTyrTrp
8581            ATTCTGGGGCACAGGGGGTGGGAAGCCCTCAAATATTGGTGGAGTCTCCTGCAGTATTGG
                TAAGACCCCGTGTCCCCCACCCTTCGGGAGTTTATAACCACCTCAGAGGACGTCATAACC

                8629 pst1,

                IleGlnGluLeuLysAsnSerAlaValSerTrpLeuAsnAlaThrAlaIleAlaValThr
8641            ATTCAGGAACTAAAGAATAGTGCTGTTAGCTGGCTCAACGCCACAGCTATAGCAGTAACT
                TAAGTCCTTGATTTCTTATCACGACAATCGACCGAGTTGCGGTGTCGATATCGTCATTGA

                GluGlyThrAspArgValIleGluValAlaGlnArgAlaTyrArgAlaIleLeuHisIle
8701            GAGGGGACAGATAGGGTTATAGAAGTAGCACAAAGAGCTTATAGAGCTATTCTCCACATA
                CTCCCCTGTCTATCCCAATATCTTCATCGTGTTTCTCGAATATCTCGATAAGAGGTGTAT

                HisArgArgIleArgGlnGlyLeuGluArgLeuLeuLeuOC  MetGlyGlyLysTrpSer
8761            CATAGAAGAATTAGACAGGGCTTGGAAAGGCTTTTGCTATAAGATGGGTGGCAAGTGGTCA
                GTATCTTCTTAATCTGTCCCGAACCTTTCCGAAAACGATATTCTACCCACCGTTCACCAGT

                8765 mbo11,

                LysArgSerMetGlyGlyTrpSerAlaIleArgGluArgMetArgArgAlaGluProArg
8822            AAACGTAGTATGGGTGGATGGTCTGCTATAAGGGAAAGAATGAGACGAGCTGAGCCACGA
                TTTGCATCATACCCACCTACCAGACGATATTCCCTTTCTTACTCTGCTCGACTCGGTGCT

                AlaGluProAlaAlaAspGlyValGlyAlaValSerArgAspLeuGluLysHisGlyAla
8882            GCTGAGCCAGCAGCAGATGGGGTGGGAGCAGTATCTCGAGACCTGGAAAAACATGGAGCA
                CGACTCGGTCGTCGTCTACCCCACCCTCGTCATAGAGCTCTGGACCTTTTTGTACCTCGT

                8883 tthIII1, 8916 ava1 xho1,

                IleThrSerSerAsnThrAlaAlaThrAsnAlaAspCysAlaTrpLeuGluAlaGlnGlu
8942            ATCACAAGTAGCAATACAGCAGCTACTAATGCTGATTGTGCCTGGCTAGAAGCACAAGAG
                TAGTGTTCATCGTTATGTCGTCGATGATTACGACTAACACGGACCGATCTTCGTGTTCTC

                GluGluGluValGlyPheProValArgProGlnValProLeuArgProMetThrTyrLys
9002            GAGGAAGAGGTGGGTTTTCCAGTCAGACCTCAGGTACCTTTAAGACCAATGACTTACAAG
                CTCCTTCTCCACCCAAAAGGTCAGTCTGGAGTCCATGGAAATTCTGGTTACTGAATGTTC

                9005 mbo11, 9029 mstII, 9034 kpn1,

                AlaAlaLeuAspIleSerHisPheLeuLysGluLysGlyGlyLeuGluGlyLeuIleTrp
9062            GCAGCTTTAGATATTAGCCACTTTTTAAAAGAAAAGGGGGGACTGGAAGGGCTAATTTGG
                CGTCGAAATCTATAATCGGTGAAAAATTTTCTTTTCCCCCCTGACCTTCCCGATTAAACC

                9085 aha111,

                SerGlnArgArgGlnGluIleLeuAspLeuTrpIleTyrHisThrGlnGlyTyrPhePro
9122            TCCCAAAGAAGACAAGAGATCCTTGATCTGTGGATCTACCACACACAAGGCTACTTCCCT
                AGGGTTTCTTCTGTTCTCTAGGAACTAGACACCTAGATGGTGTGTGTTCCGATGAAGGGA

                9129 mbo11, 9153 binI,

                AspTrpGlnAsnTyrThrProGlyProGlyIleArgTyrProLeuThrPheGlyTrpCys
9182            GATTGGCAGAATTACACACCAGGGCCAGGGATCAGATATCCACTGACCTTTGGATGGTGC
                CTAACCGTCTTAATGTGTGGTCCCGGTCCCTAGTCTATAGGTGACTGGAAACCTACCACG

                9210 binI, 9216 ecor5,

                PheLysLeuValProValGluProGluLysValGluGluAlaAsnGluGlyGluAsnAsn
9242            TTCAAGCTAGTACCAGTTGAGCCAGAGAAGGTAGAAGAGGCCAATGAAGGAGAGAACAAC
                AAGTTCGATCATGGTCAACTCGGTCTCTTCCATCTTCTCCGGTTACTTCCTCTCTTGTTG

                9275 mbo11,

                SerLeuLeuHisProMetSerLeuHisGlyMetGluAspAlaGluLysGluValLeuVal
9302            AGCTTGTTACACCCTATGAGCCTGCATGGGATGGAGGACGCGGAGAAAGAAGTGTTAGTG
                TCGAACAATGTGGGATACTCGGACGTACCCTACCTCCTGCGCCTCTTTCTTCACAATCAC

                TrpArgPheAspSerLysLeuAlaPheHisHisMetAlaArgGluLeuHisProGluTyr
9362            TGGAGGTTTGACAGCAAACTAGCATTTCATCACATGGCCCGAGAGCTGCATCCGGAGTAC
                ACCTCCAAACTGTCGTTTGATCGTAAAGTAGTGTACCGGGCTCTCGACGTAGGCCTCATG

                9399 ava1, 9417 sca1,

                TyrLysAspCysOP
9422            TACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCCGCTGGGGACTTTCCAGGG
                ATGTTTCTGACGACTGTAGCTCGAAAGATGTTCCCTGAAAGGCGACCCCTGAAAGGTCCC

9482            AGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGTCCCTCAGATGCTGCATATAAGCAGCTG
                TCCGCACCGGACCCGCCCTGACCCCTCACCGCAGGGAGTCTACGACGTATATTCGTCGAC

                9536 pvu11,
```

CONFIDENTIAL

Figure 4
Page 12 of 12

```
9542  CTTTTTGCCTGTACTGGGTCTC  GGTTAGACCAGATCTGAGCCTGGGAGC TCTGGC
      GAAAAACGGACATGACCCAGAGAGACCAATCTGGTCTAGACTCGGACCCTCGAGAGACCG

      9576 bglii, 9590 sacI,

9602  TAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAGTGCTTCAAGTAGTG
      ATTGATCCCTTGGGTGACGAATTCGGAGTTATTTCGAACGGAACTCACGAAGTTCATCAC

      9620 afIII, 9634 hindIII,

9662  TGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTAGTCAGTG
      ACACGGGCAGACAACACACTGAGACCATTGATCTCTAGGGAGTCTGGGAAAATCAGTCAC

9722  TGGAAAAATCTCTAGCAG
      ACCTTTTTAGAGATCGTC
```




LTR

GAG

POL

CONFIDENTIAL

08/288336

FIGURE 5
1 of 4

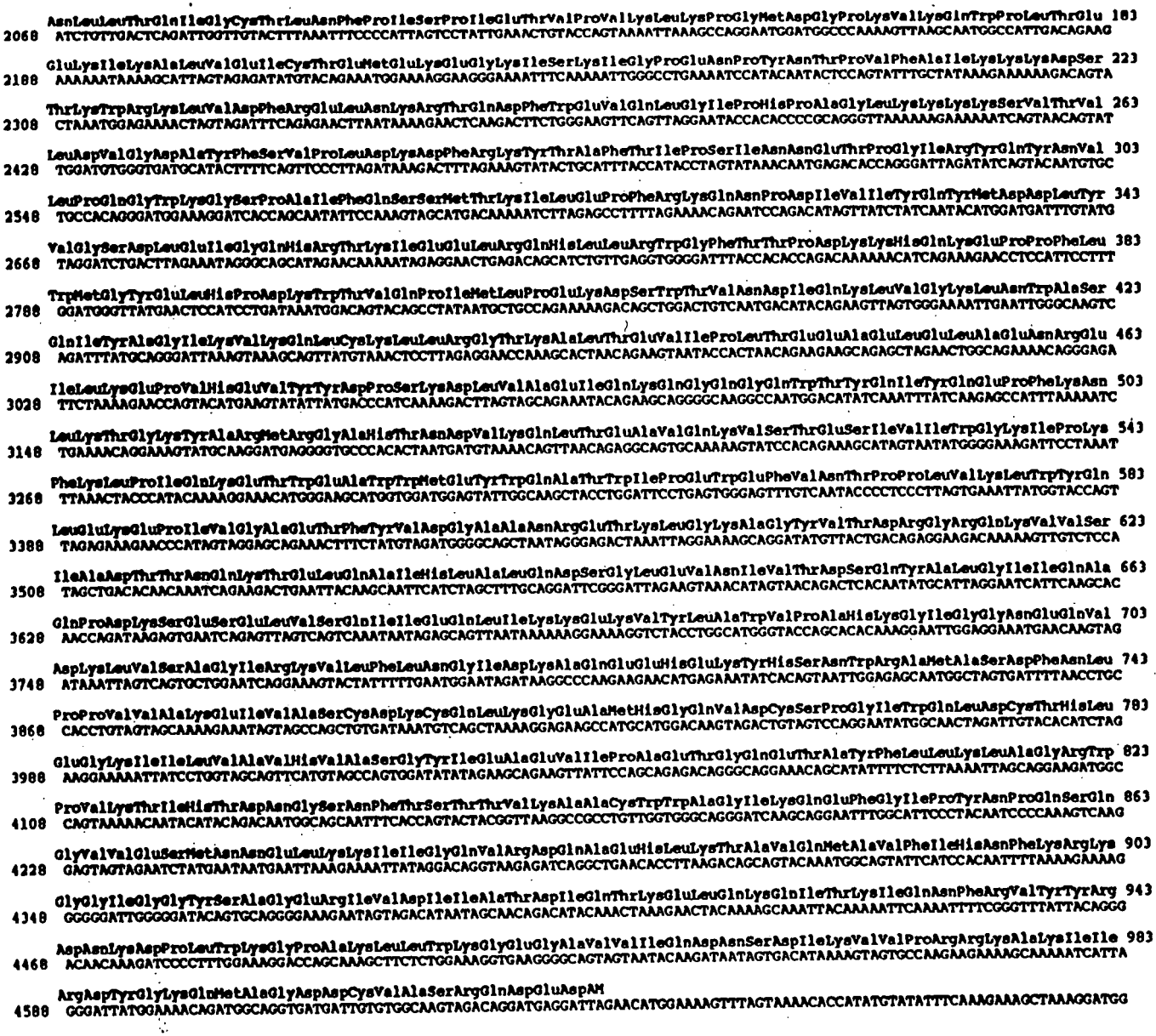



FIGURE 5
2 of 4

POL

CONFIDENTIAL

08/288336

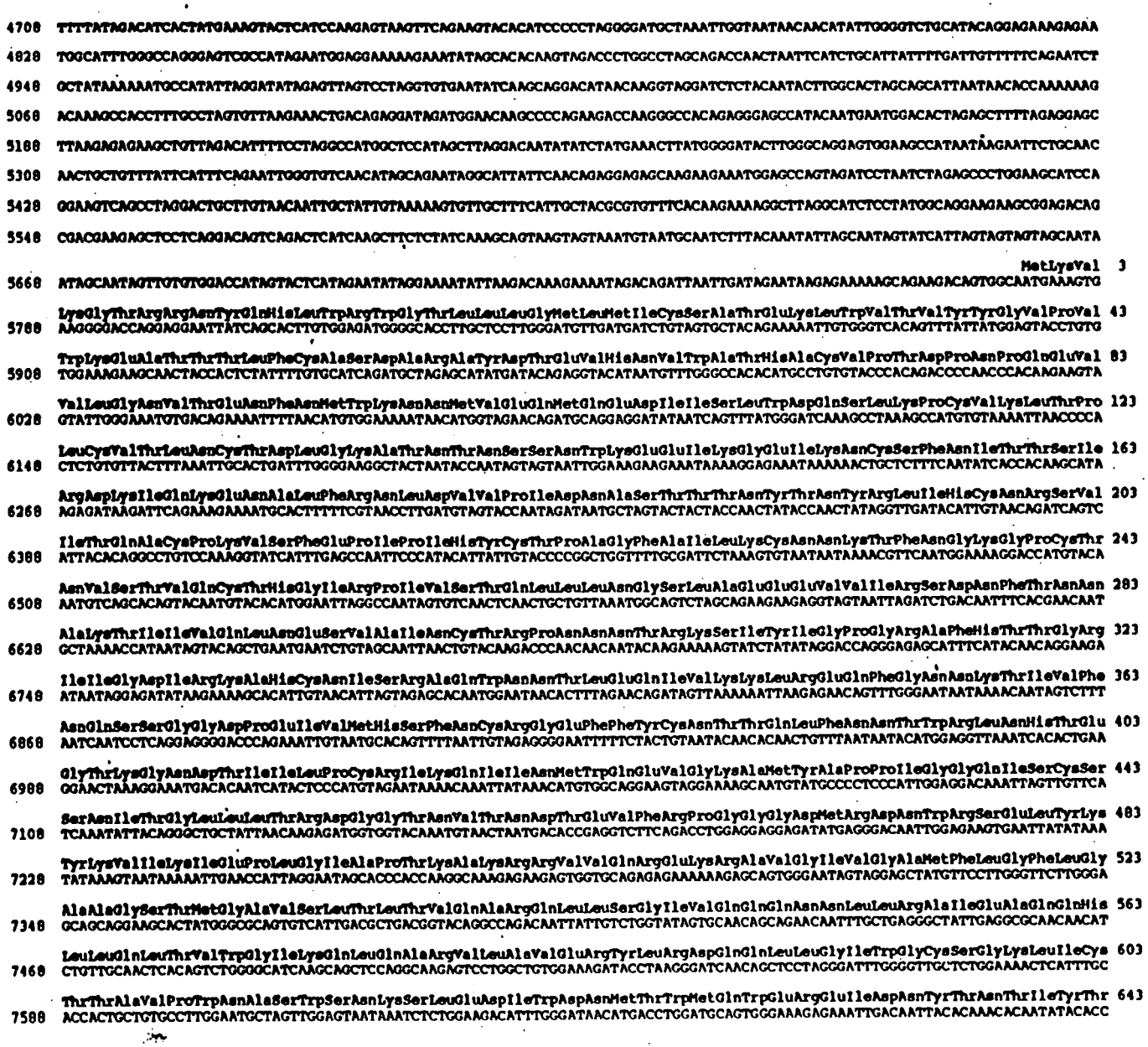


FIGURE 5
3 of 4

E 7
CONFIDENTIAL
08/288336


FIGURE 5
4 of 4

ENV

LTR

CONFIDENTIAL

08/288336

CONFIDENTIAL

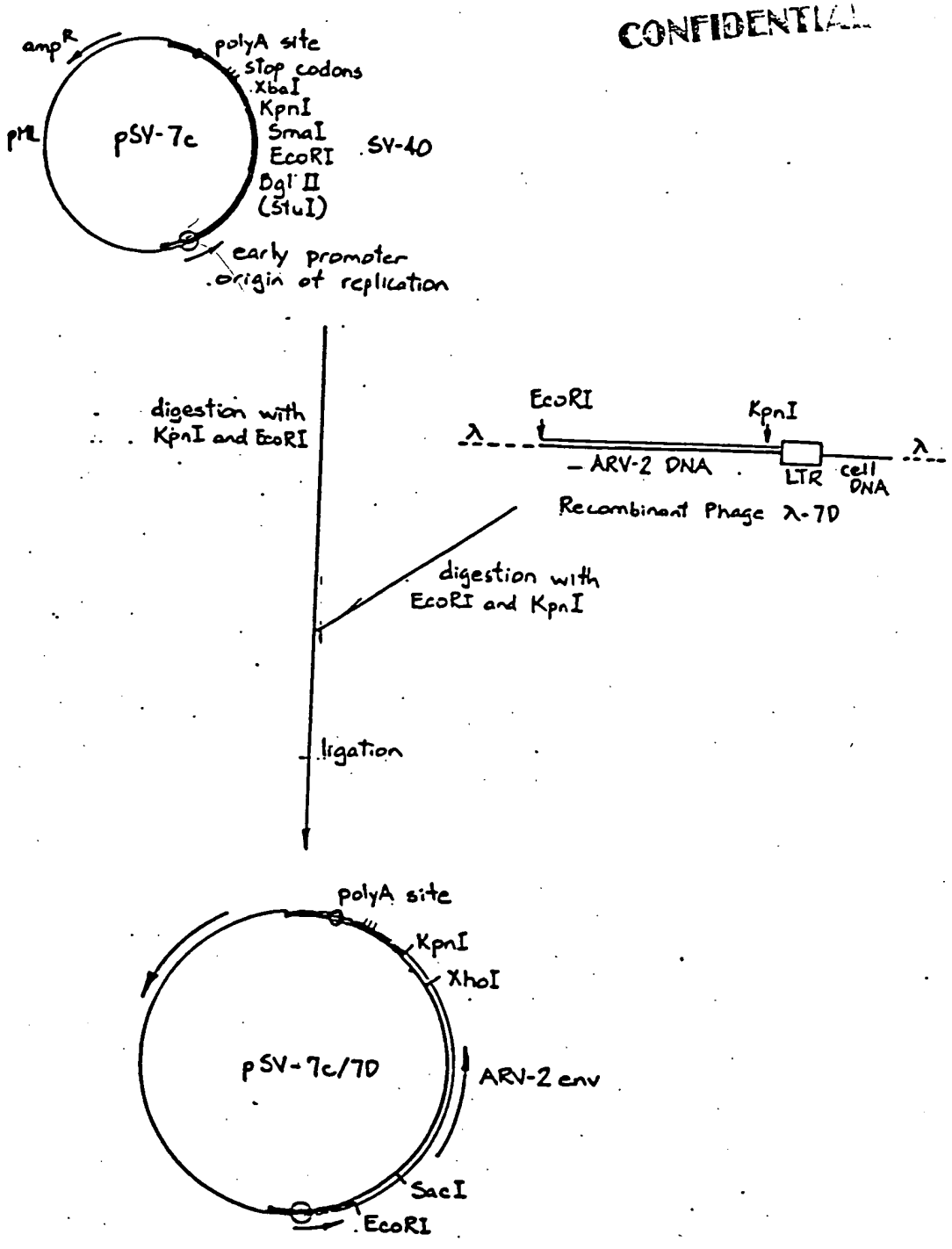
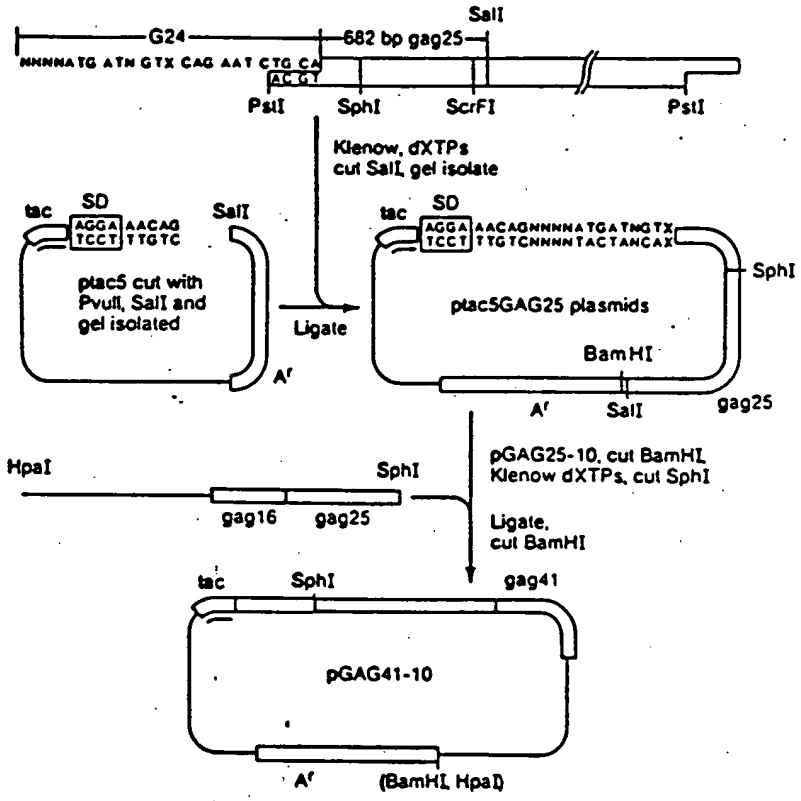


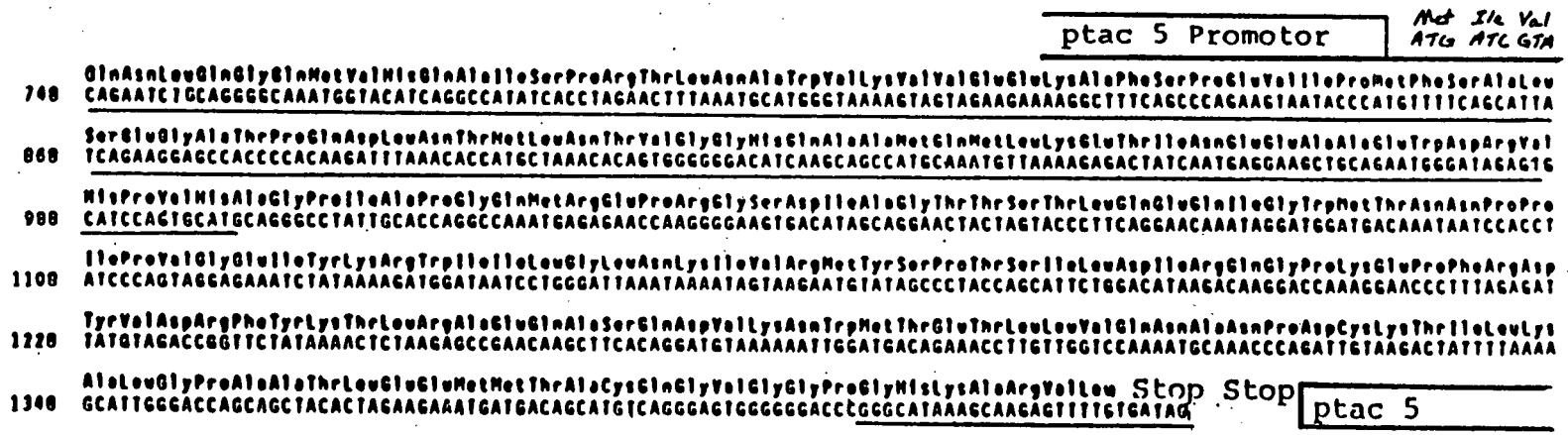

FIG. 6

CONFIDENTIAL

Figure 7



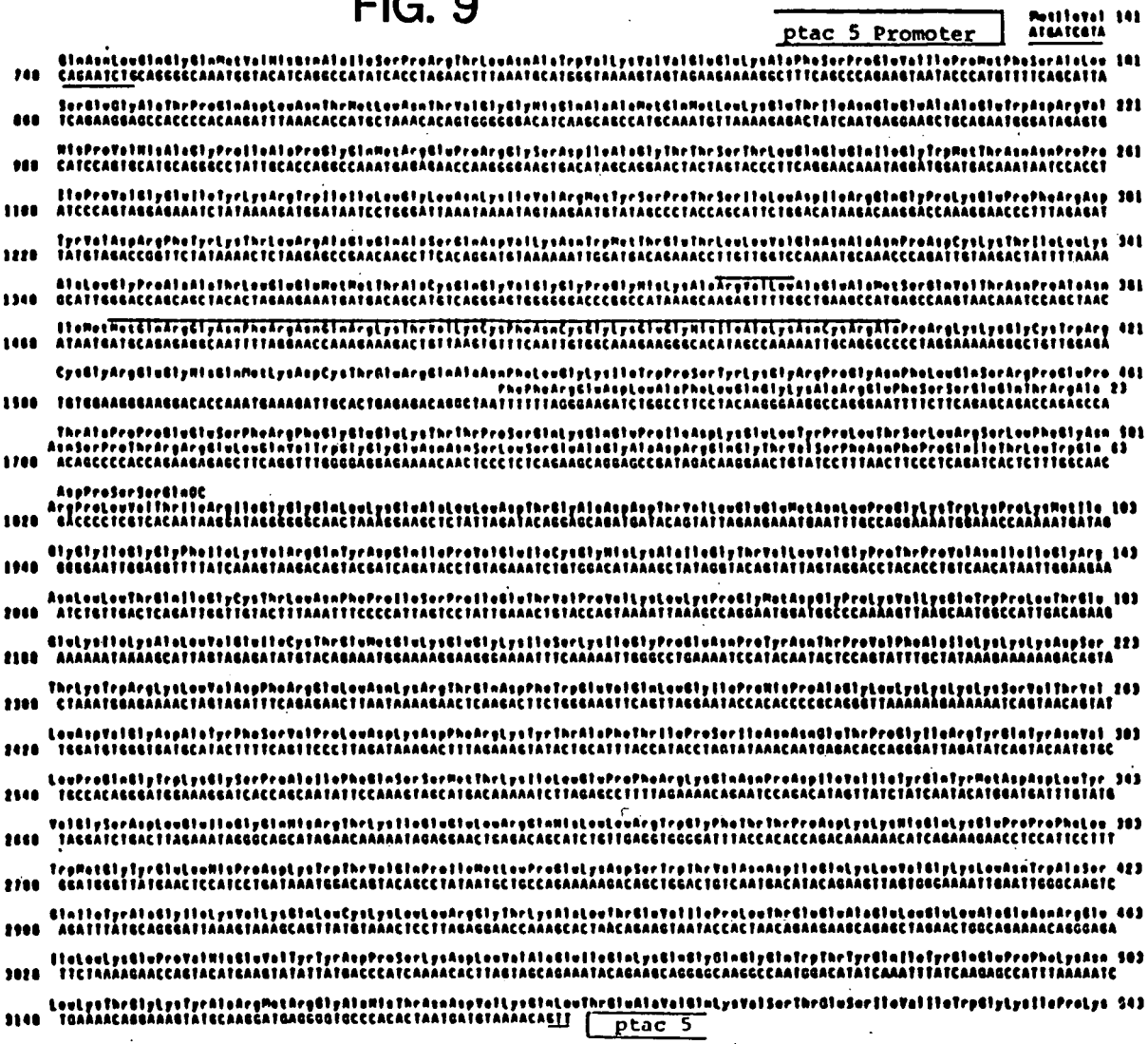
# FIG. 8




CONFIDENTIAL

08/288336

# FIG. 9

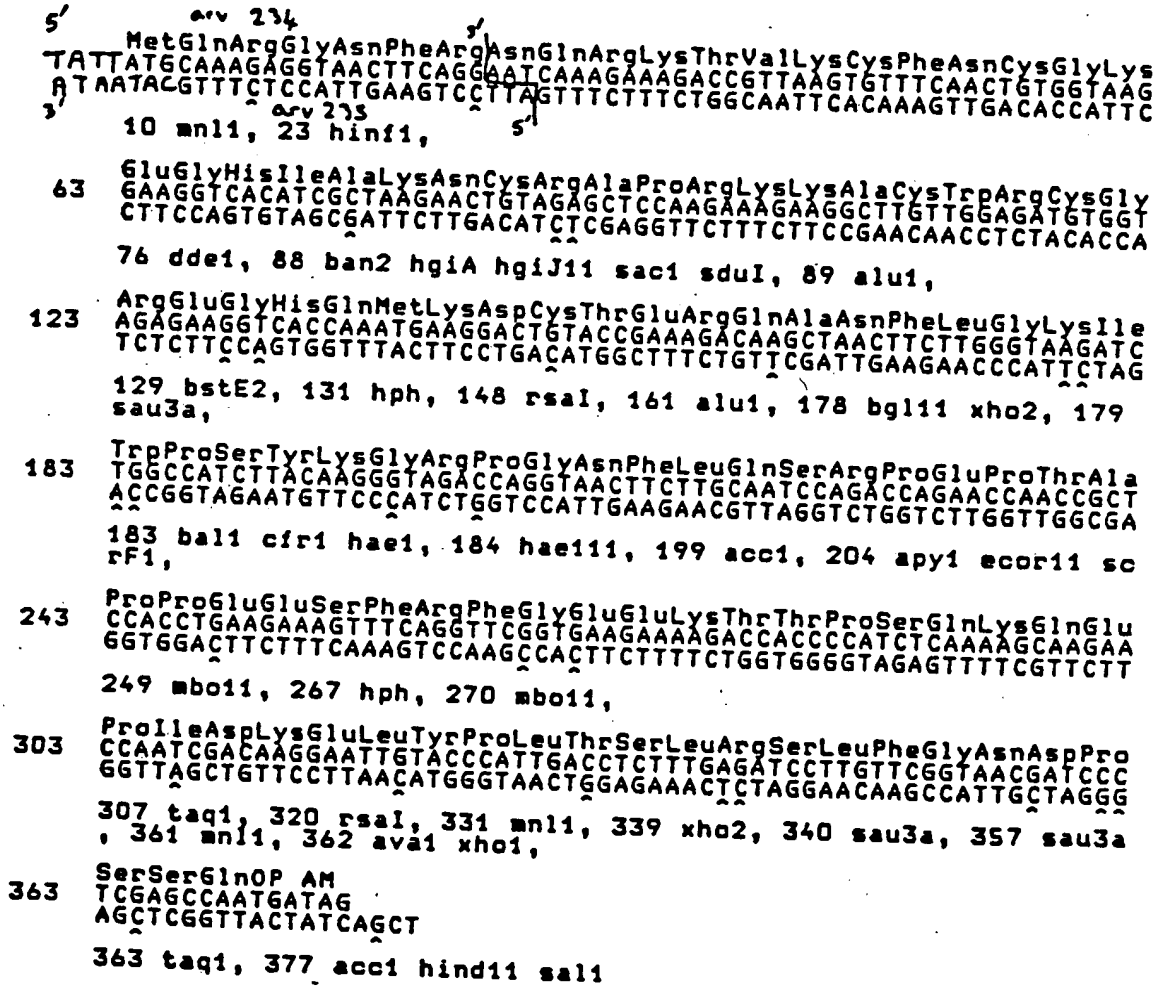



CONFIDENTIAL

CONFIDENTIAL

Figure 10

ARV GAG p16 - synthetic Parts A and B



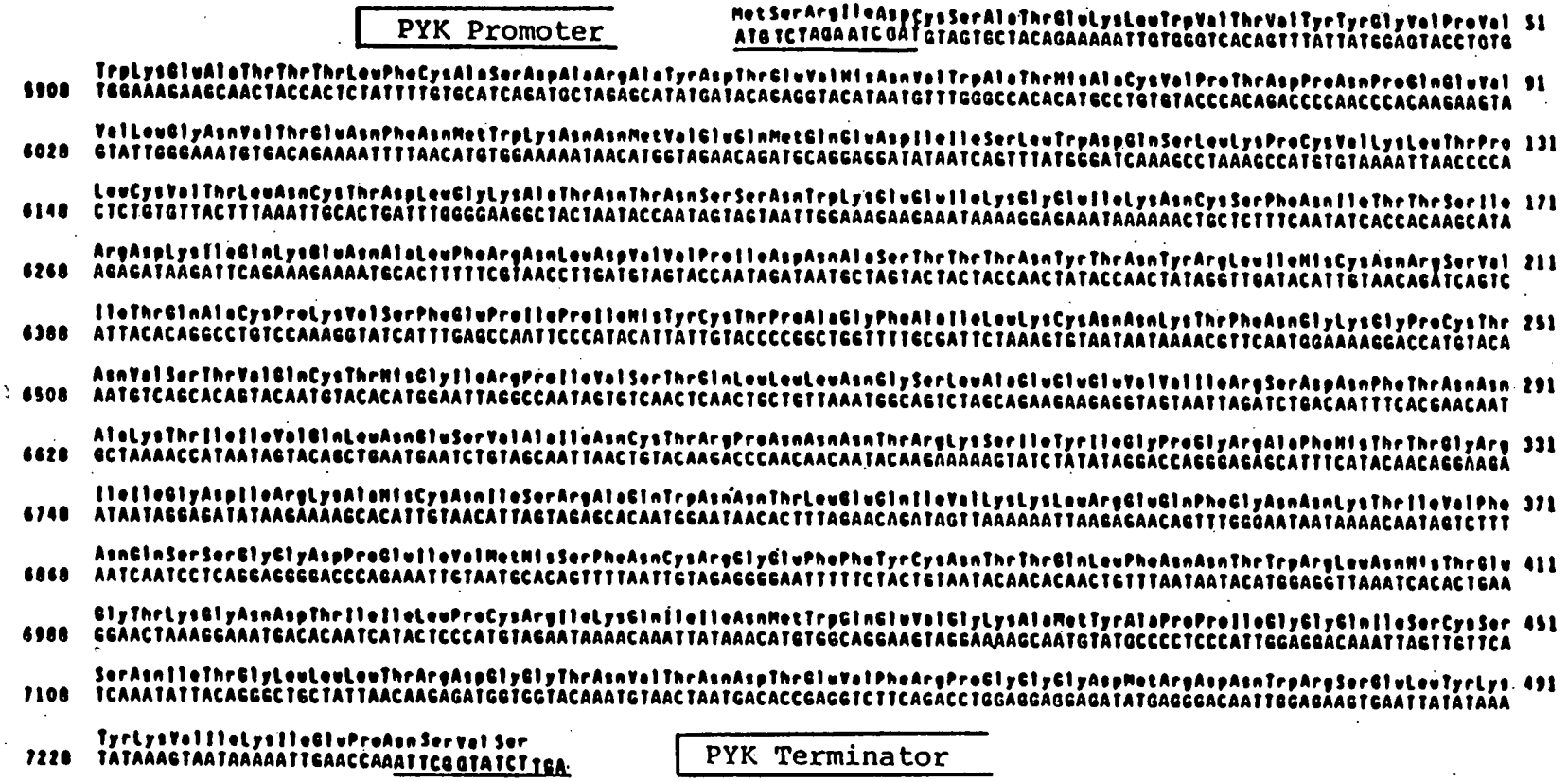



FIG. 11

ENV
CONFIDENTIAL
08/288336

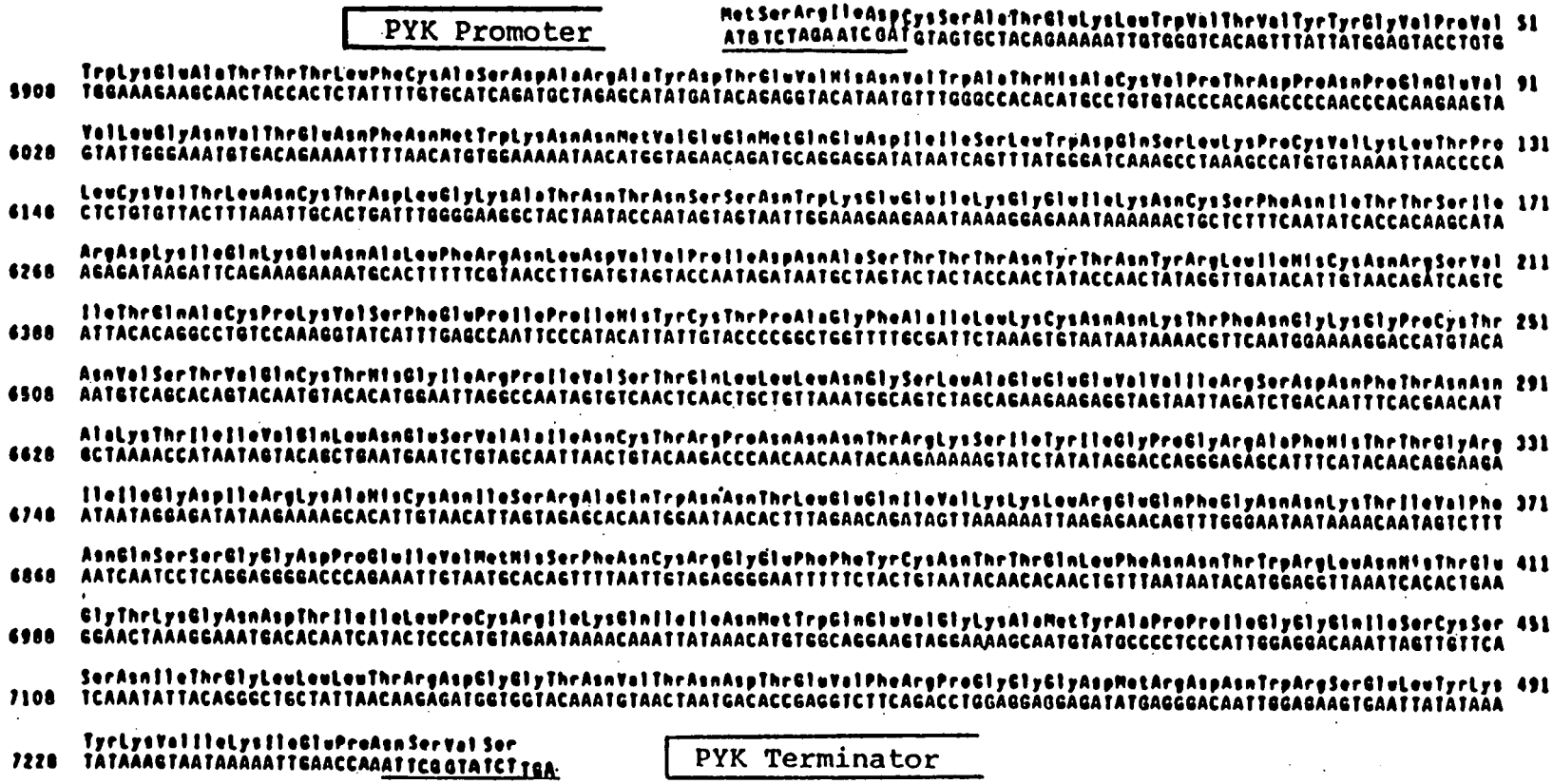



FIG. 11

ENV CONFIDENTIAL

08/280,330

FIGURE 12



CONFIDENTIAL

Nucleotide positions relative to FIGURE 5.

```
                                                MetIleAspLysAlaGlnGluGluHisGluLysTyrHisSerAsnTrp
      1 AGGXAACAG::::ATGAT:GA:AAGGCACAAGAAGAACATGAGAAATATCACAGTAATTGG
        TCCXTTGTC::::TACTA:CT:TTCCGTGTTCTTCTTGTACTCTTTATAGTGTCATTAACC

        32 mbo11, 38 nla111,

        ArgAlaMetAlaSerAspPheAsnLeuProProValValAlaLysGluIleValAlaSer
 3820  62 AGAGCCATGGCTAGTGATTTTAACCTGCCACCTGTAGTAGCAAAAGAAATAGTAGCCAGC
        TCTCGGTACCGATCACTAAAATTGGACGGTGGACATCATCGTTTTCTTTATCATCGGTCG

        66 nco1, 67 nla111, 118 nspBII pvu11, 119 alu1,

        CysAspLysCysGlnLeuLysGlyGluAlaMetHisGlyGlnValAspCysSerProGly
 3880 122 TGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGACTGTAGTCCAGGA
        ACACTATTTACAGTCGATTTTCCTCTTCGGTACGTACCTGTTCATCTGACATCAGGTCCT

        135 alu1, 151 nla111, 152 nsi1 ava3, 155 nla111, 164 acc1, 1
        76 apy1 bstXI ecor11 scrF1,

        IleTrpGlnLeuAspCysThrHisLeuGluGlyLysIleIleLeuValAlaValHisVal
 3940 182 ATATGGCAACTAGATTGTACACATCTAGAAGGAAAAATTATCCTGGTAGCAGTTCATGTA
        TATACCGTTGATCTAACATGTGTAGATCTTCCTTTTTAATAGGACCATCGTCAAGTACAT

        198 rsaI, 205 xba1, 223 apy1 ecor11 scrF1, 236 nla111,

        AlaSerGlyTyrIleGluAlaGluValIleProAlaGluThrGlyGlnGluThrAlaTyr
 4000 242 GCCAGTGGATATATAGAAGCAGAAGTTATTCCAGCAGAGACAGGGCAGGAAACAGCATAT
        CGGTCACCTATATATCTTCGTCTTCAATAAGGTCGTCTCTGTCCCGTCCTTTGTCGTATA

        263 xmn1,

        PheLeuLeuLysLeuAlaGlyArgTrpProValLysThrIleHisThrAspAsnGlySer
 4060 302 TTTCTCTTAAAATTAGCAGGAAGATGGCCAGTAAAAACAATACATACAGACAATGGCAGC
        AAAGAGAATTTTAATCGTCCTTCTACCGGTCATTTTTGTTATGTATGTCTGTTACCGTCG

        321 mbo11, 326 bal1 cfr1 hae1, 327 hae111, 357 bbv fnu4h1,

        AsnPheThrSerThrThrValLysAlaAlaCysTrpTrpAlaGlyIleLysGlnGluPhe
 4120 362 AATTTCACCAGTACTACGGTTAAGGCCGCCTGTTGGTGGGCAGGGATCAAGCAGGAATTT
        TTAAAGTGGTCATGATGCCAATTCCGGCGGACAACCACCCGTCCCTAGTTCGTCCTTAAA

        366 hph, 371 sca1, 372 rsaI, 385 hae111, 386 fnu4h1 nsb11, 4
        05 bin1, 406 dpn1 sau3a,

        GlyIleProTyrAsnProGlnSerGlnGlyValValGluSerMetAsnAsnGluLeuLys
 4180 422 GGCATTCCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTATGAATAATGAATTAAAG
        CCGTAAGGGATGTTAGGGGTTTCAGTTCCTCATCATCTTAGATACTTATTACTTAATTTC

        423 bsm1, 458 hinf1,

        LysIleIleGlyGlnValArgAspGlnAlaGluHisLeuLysThrAlaValGlnMetAla
 4240 482 AAAATTATAGGACAGGTAAGAGATCAGGCTGAACACCTTAAGACAGCAGTACAAATGGCA
        TTTTAATATCCTGTCCATTCTCTAGTCCGACTTGTGGAATTCTGTCGTCATGTTTACCGT

        503 dpn1 sau3a, 518 afl11, 530 rsaI,

        ValPheIleHisAsnPheLysArgLysGlyGlyIleGlyGlyTyrSerAlaGlyGluArg
 4300 542 GTATTCATCCACAATTTTAAAAGAAAAGGGGGGATTGGGGGATACAGTGCAGGGGAAAGA
        CATAAGTAGGTGTTAAAATTTTCTTTTCCCCCCTAACCCCCTATGTCACGTCCCCTTTCT

        547 fok1, 557 aha111,

        IleValAspIleIleAlaThrAspIleGlnThrLysGluLeuGlnLysGlnIleThrLys
 4360 602 ATAGTAGACATAATAGCAACAGACATACAAACTAAAGAACTACAAAAGCAAATTACAAAA
        TATCATCTGTATTATCGTTGTCTGTATGTTTGATTTCTTGATGTTTTCGTTTAATGTTTT

        605 acc1,

        IleGlnAsnPheArgValTyrTyrArgAspAsnLysAspProLeuTrpLysGlyProAla
      662 ATTCAAAATTTTCGGGTTTATTACAGGGACAACAAAGATCCCCTTTGGAAAGGACCAGCA
```

CONFIDENTIAL

4480 722 LysLeuLeuTrpLysGlyGluGlyAlaValValIleGlnAspAsnSerAspIleLysVal
AAGCTTCTCTGGAAAGGTGAAGGGGCAGTAGTAATACAAGATAATAGTGACATAAAAGTA
TTCGAAGAGACCTTTCCACTTCCCCGTCATCATTATGTTCTATTATCACTGTATTTTCAT

722 hind111, 723 alu1, 737 hph,

4540 782 ValProArgArgLysAlaLysIleIleArgAspTyrGlyLysGlnMetAlaGlyAspAsp
GTGCCAAGAAGAAAAGCAAAAATCATTAGGGATTATGGAAAACAGATGGCAGGTGATGAT
CACGGTTCTTCTTTTCGTTTTTAGTAATCCCTAATACCTTTTGTCTACCGTCCACTACTA

789 mbo11, 833 hph,

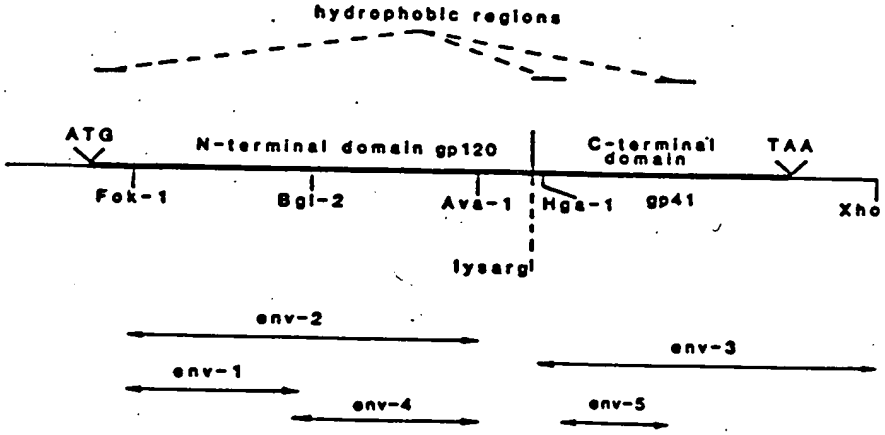
4600 842 CysValAlaSerArgGlnAspGluAspAM
TGTGTGGCAAGTAGACAGGATGAGGATTAGTCGACGGAATTCTTTAGTAAAACACC
ACACACCGTTCATCTGTCCTACTCCTAATCAGCTGCCTTAAGAAATCATTTTGTGG

852 acc1, 859 fok1, 863 mnl1, 871 acc1 hind11 sal1, 872 taq1
, 878 ecor1,

FIGURE 12

2 of 2

CONFIDENTIAL




env expression in yeast and bacteria

FIGURE 13

CONFIDENTIAL

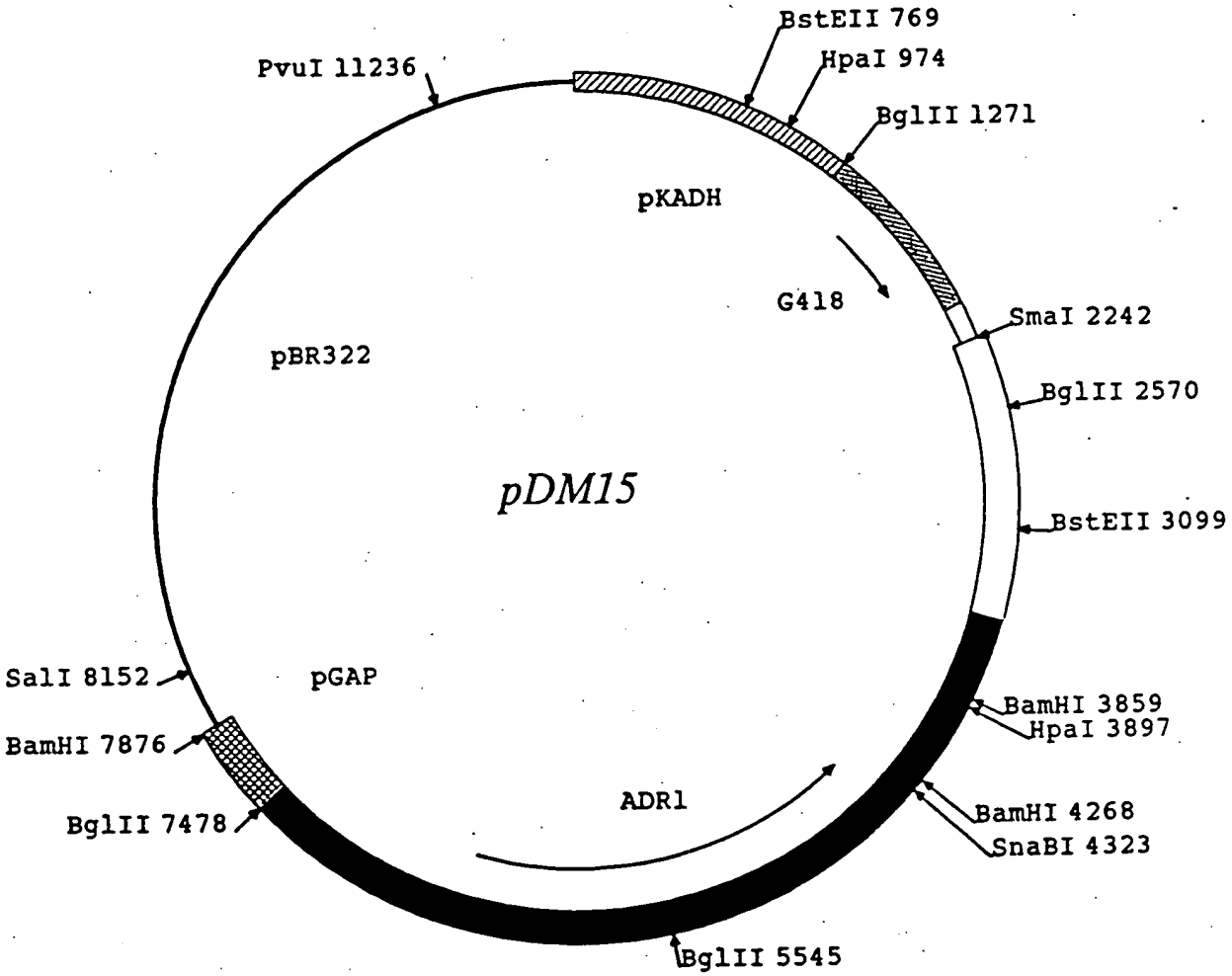



FIGURE 14

CONFIDENTIAL

SCD

```
   MetAlaThrLysAlaValCysValLeuLysGlyAspGlyProValGlnGlyIleIleAsn
 1 CATGGCGACGAAGGCCGTGTGCGTCTGAAGGGCGACGGCCCAGTGCAGGGCATCATCAAT
     CGCTGCTTCCGGCACACGCACGACTTCCCGCTGCCGGGTCACGTCCCGTAGTAGTTA

   PheGluGlnLysGluSerAsnGlyProValLysValTrpGlySerIleLysGlyLeuThr
62 TTCGAGCAGAAGGAAAGTAATGGACCAGTGAAGGTGTGGGGAAGCATTAAAGGACTGACT
   AAGCTCGTCTTCCTTTCATTACCTGGTCACTTCCACACCCCTTCGTAATTTCCTGACTGA

   GluGlyLeuHisGlyPheHisValHisGluPheGlyAspAsnThrAlaGlyCysThrSer
122 GAAGGCCTGCATGGATTCCATGTTCATGAGTTTGGAGATAATACAGCAGGCTGTACCAGT
    CTTCCGGACGTACCTAAGGTACAAGTACTCAAACCTCTATTATGTCGTCCGACATGGTCA

   AlaGlyProHisPheAsnProLeuSerArgLysHisGlyGlyProLysAspGluGluArg
182 GCAGGTCCTCACTTTAATCCTCTATCCAGAAAACACGGTGGGCCAAAGGATGAAGAGAGG
    CGTCCAGGAGTGAAATTAGGAGATAGGTCTTTTGTGCCACCCGGTTTCCTACTTCTCTCC

   HisValGlyAspLeuGlyAsnValThrAlaAspLysAspGlyValAlaAspValSerIle
242 CATGTTGGAGACTTGGGCAATGTGACTGCTGACAAAGATGGTGTGGCCGATGTGTCTATT
    GTACAACCTCTGAACCCGTTACACTGACGACTGTTTCTACCACACCGGCTACACAGATAA

   GluAspSerValIleSerLeuSerGlyAspHisCysIleIleGlyArgThrLeuValVal
302 GAAGATTCTGTGATCTCACTCTCAGGAGACCATTGCATCATTGGCCGCACACTGGTGGTC
    CTTCTAAGACACTAGAGTGAGAGTCCTCTGGTAACGTAGTAACCGGCGTGTGACCACCAG

   HisGluLysAlaAspAspLeuGlyLysGlyGlyAsnGluGluSerThrLysThrGlyAsn
362 CATGAAAAAGCAGATGACTTGGGCAAAGGTGGAAATGAAGAAAGTACAAAGACAGGAAAC
    GTACTTTTTCGTCTACTGAACCCGTTTCCACCTTTACTTCTTTCATGTTTCTGTCCTTTG

                                                    ENV SB
   AlaGlySerArgLeuAlaCysGlyValIleGlyIleAlaMetAlaIleGluAlaGlnGln
422 GCTGGAAGTCGTTTGGCTTGTGGTGTAATTGGGATCGCCATGGCTATCGAAGCTCAACAA
    CGACCTTCAGCAAACCGAACACCACATTAACCCTAGCGGTACCGATAGCTTCGAGTTGTT
                                                    401

   HisLeuLeuGlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgValLeuAlaVal
482 CACTTGCTGCAGTTGACCGTTTGGGGTATCAAGCAGTTGCAGGCTAGAGTTTTGGCTGTT
    GTGAACGACGTCAACTGGCAAACCCCATAGTTCGTCAACGTCCGATCTCAAAACCGACAA

   GluArgTyrLeuArgAspGlnGlnLeuLeuGlyIleTrpGlyCysSerGlyLysLeuIle
542 GAAAGATACTTGAGAGATCAACAATTGTTGGGTATCTGGGGTTGTTCTGGTAAGTTGATT
    CTTTCTATGAACTCTCTAGTTGTTAACAACCCATAGACCCCAACAAGACCATTCAACTAA

   CysThrThrAlaValProTrpAsnAlaSerTrpSerAsnLysSerLeuGluAspIleTrp
602 TGTACCACCGCTGTTCCCTGGAACGCTTCTTGGTCTAACAAGTCTTTGGAAGACATCTGG
    ACATGGTGGCGACAAGGGACCTTGCGAAGAACCAGATTGTTCAGAAACCTTCTGTAGACC

   AspAsnMetThrTrpMetGlnTrpGluArgGluIleAspAsnTyrThrAsnThrIleTyr
662 GACAACATGACCTGGATGCAATGGGAAAGAGAAATCGACAACTACACCAACACCATCTAC
    CTGTTGTACTGGACCTACGTTACCCTTTCTCTTTAGCTGTTGATGTGGTTGTGGTAGATG

   ThrLeuLeuGluGluSerGlnAsnGlnGlnGluLysAsnGluGlnGluLeuLeuGluLeu
722 ACCTTGTTGGAGGAATCTCAAAACCAACAAGAAAAGAACGAACAAGAATTGTTGGAATTG
    TGGAACAACCTCCTTAGAGTTTTGGTTGTTCTTTTCTTGCTTGTTCTTAACAACCTTAAC

   AspLysTrpAlaSerLeuTrpAsnTrpPheSerIleThrAsnTrpAM
782 GACAAGTGGGCAAGCTTGTGGAACTGGTTCTCTATCACCAACTGGTAG
    CTGTTCACCCGTTCGAACACCTTGACCAAGAGATAGTGGTTGACCATCAGCT
```

Translated Mol. Weight = 30414.22

FIGURE 15

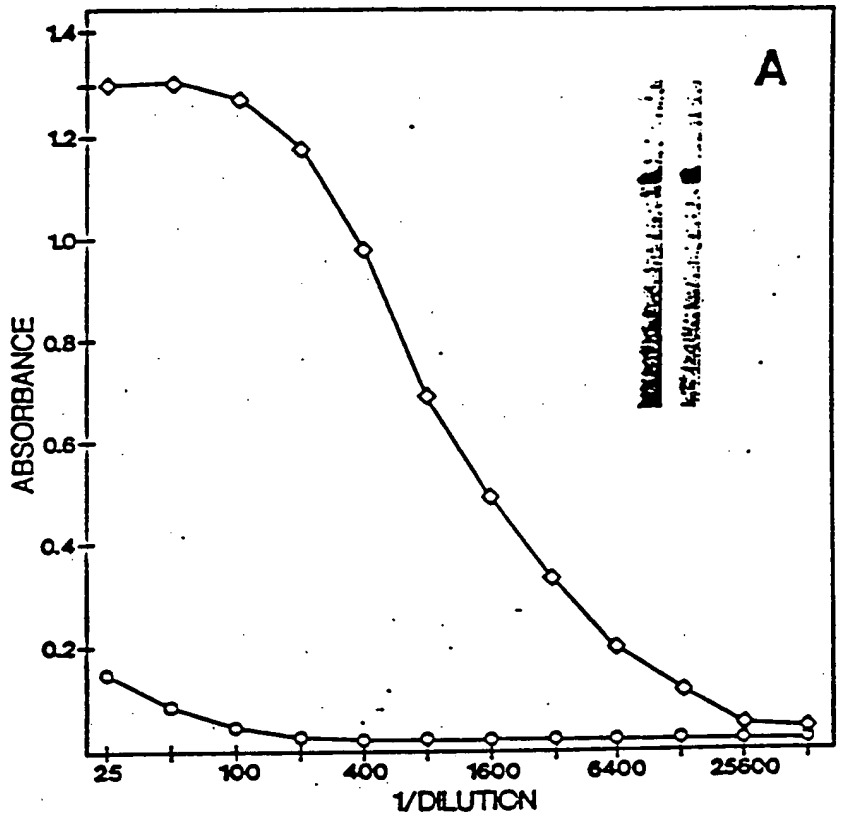

A
ABSORBANCE
1.4
1.2
1.0
0.8
0.6
0.4
0.2
25
100
400
1600
6400
25600
1/DILUTION

FIGURE 16

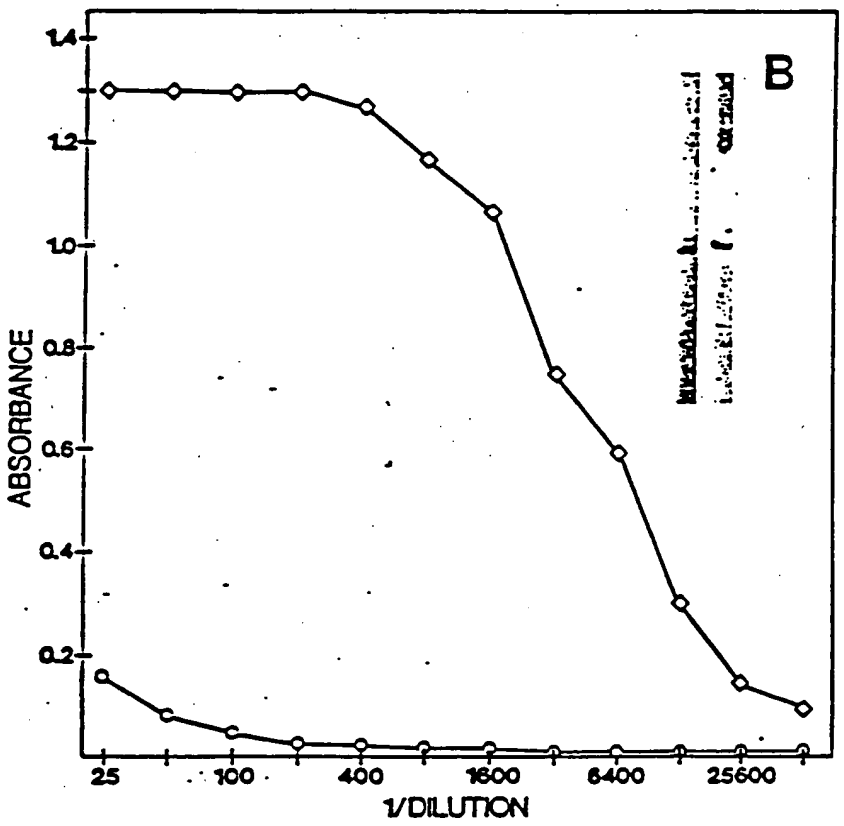



FIGURE 16

2 of 2

CONFIDENTIAL

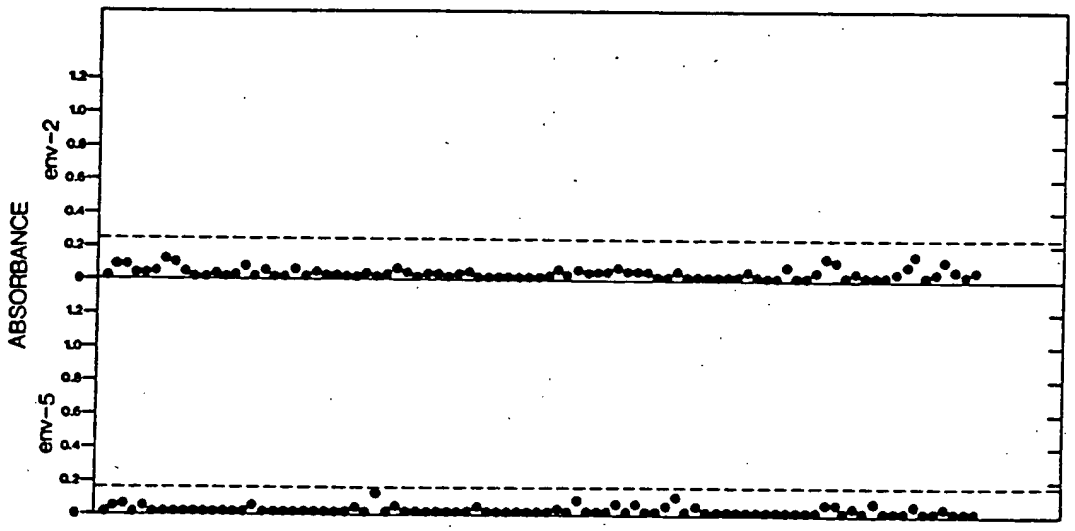



FIGURE 17

CONFIDENTIAL

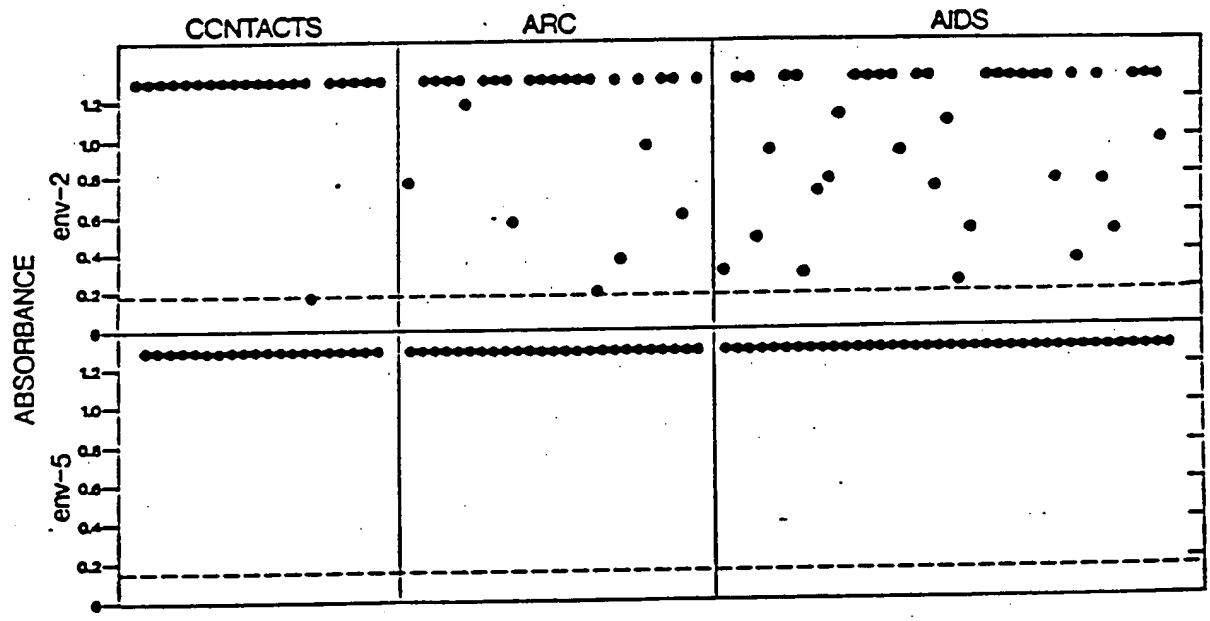



FIGURE 18

CONFIDENTIAL

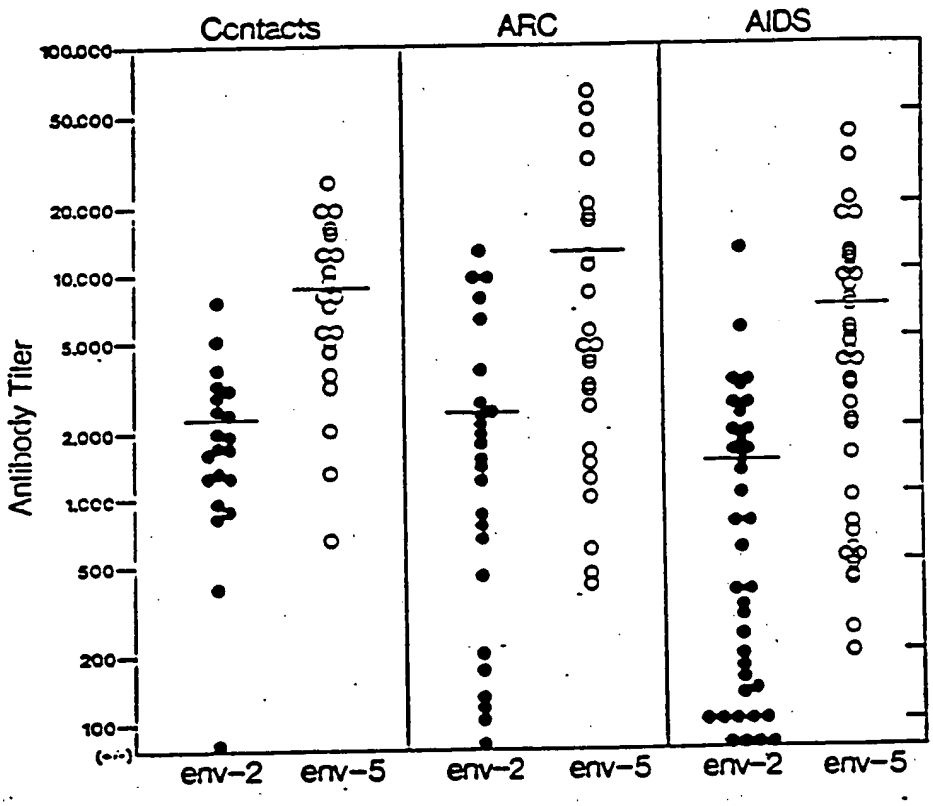



FIGURE 19

CONFIDENTIAL

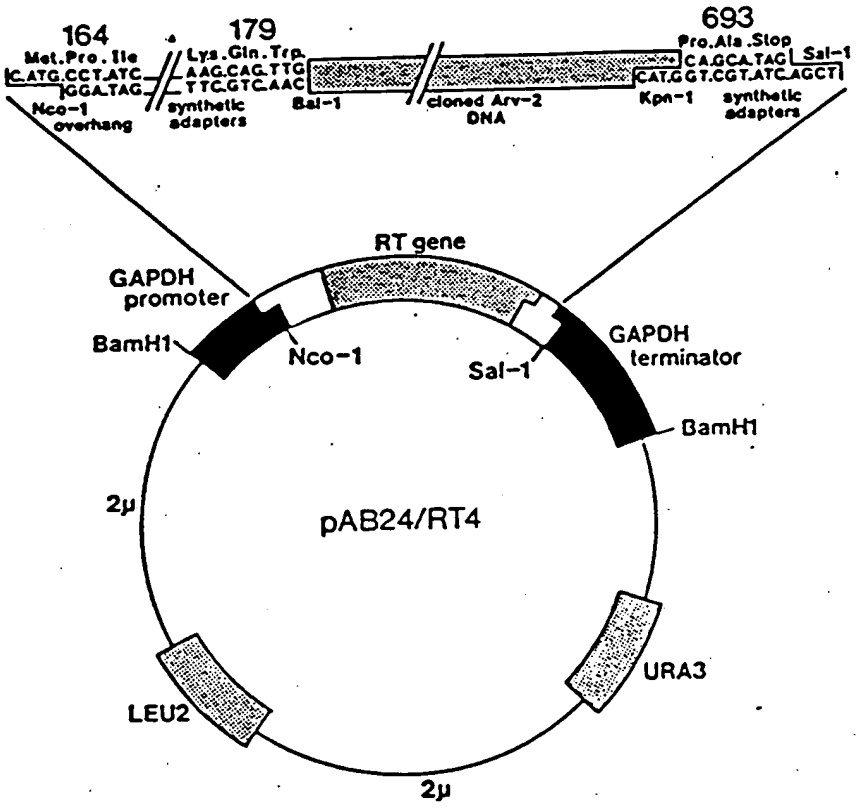



FIGURE 20

CONFIDENTIAL

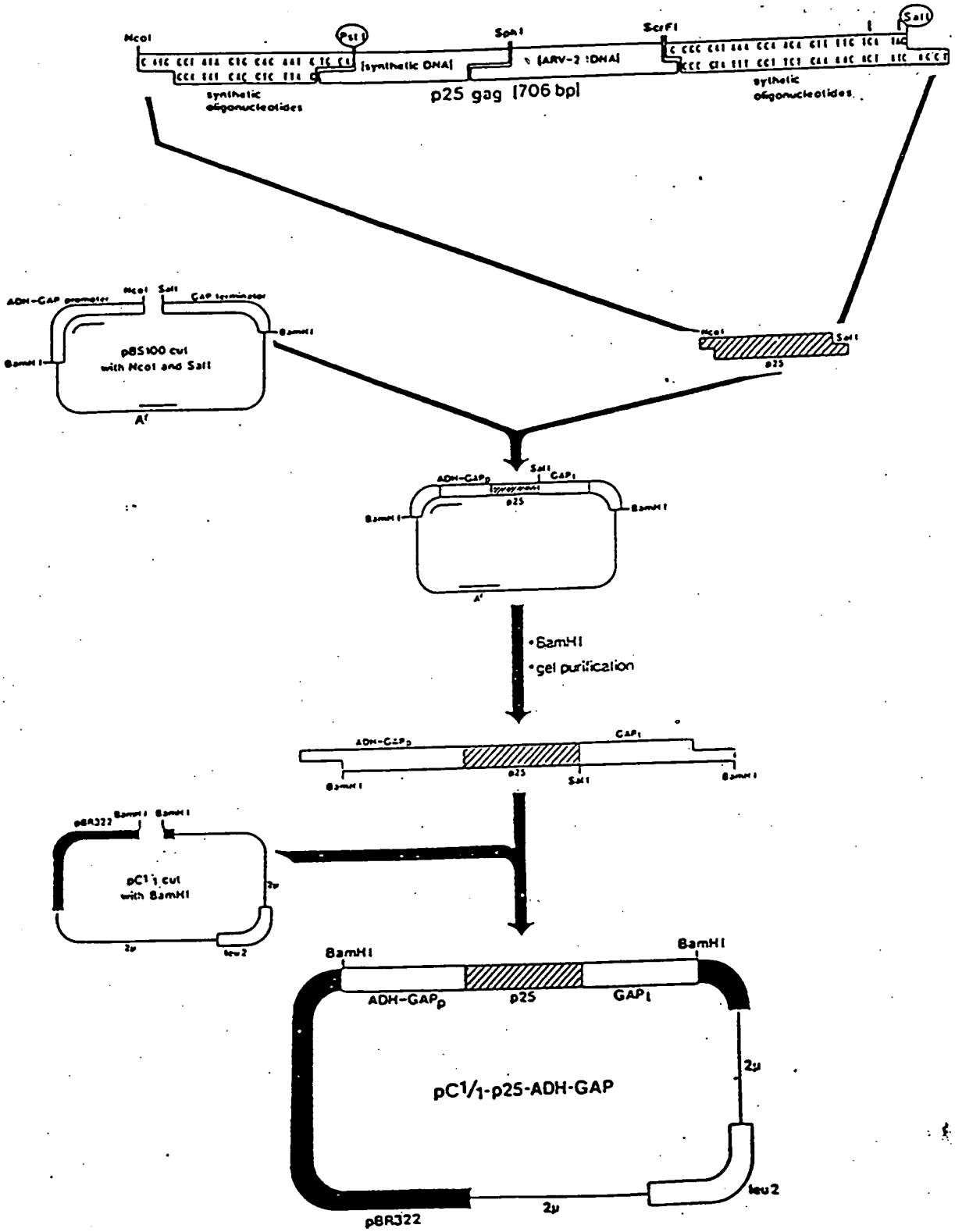



FIGURE 21

CONFIDENTIAL

```
                                                                  10
     Met Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln
C    ATG CCT ATA GTG CAG AAT CTG CAG GGG CAA ATG GTA CAT CAG

                          20
Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
GCC ATA TCA CCT AGA ACT TTA AAT GCT TGG GTA AAA GTA GTA GAA

 30                                                       40
Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
GAA AAG GCT TTC AGC CCA GAA GTA ATA CCC ATG TTT TCA GCA TTA

                          50
Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
TCA GAA GGA GCC ACC CCT CAA GAT TTA AAC ACC ATG CTA AAC ACA

 60                                                       70
Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile
GTG GGG GGA CAT CAA GCA GCC ATG CAA ATG TTA AAA GAG ACT ATC

                          80
Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala
AAT GAG GAG GCT GCC GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA

 90                                                      100
Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp
GGG CCT ATT GCA CCA GGC CAA ATG AGA GAA CCA AGG GGA AGT GAC

                         110
Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
ATA GCA GGA ACT ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG

120                                                      130
Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp
ACA AAT AAT CCA CCT ATC CCA GTA GGA GAA ATC TAT AAA AGA TGG

                         140
Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr
ATA ATC CTG GGA TTA AAT AAA ATA GTA AGA ATG TAT AGC CCT ACC

150                                                      160
Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp
AGC ATT CTG GAC ATA AGA CAA GGA CCA AAG GAA CCC TTT AGA GAT

                         170
Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser
TAT GTA GAC CGG TTC TAT AAA ACT CTA AGA GCC GAA CAA GCT TCA

180                                                      190
Gln Asp Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn
CAG GAT GTA AAA AAT TGG ATG ACA GAA ACC TTG TTG GTC CAA AAT

                         200
Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala
GCA AAC CCA GAT TGT AAG ACT ATT TTA AAA GCA TTG GGA CCA GCA

210                                                      220
Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
GCT ACA CTA GAA GAA ATG ATG ACA GCA TGT CAG GGA GTG GGG GGA

                         230      232
Pro Gly His Lys Ala Arg Val Leu OP
CCC GGG CAT AAA GCA AGA GTT TTG TGA TAG

Translated Mol. Weight = 25700.75
```

FIGURE 22

CONFIDENTIAL

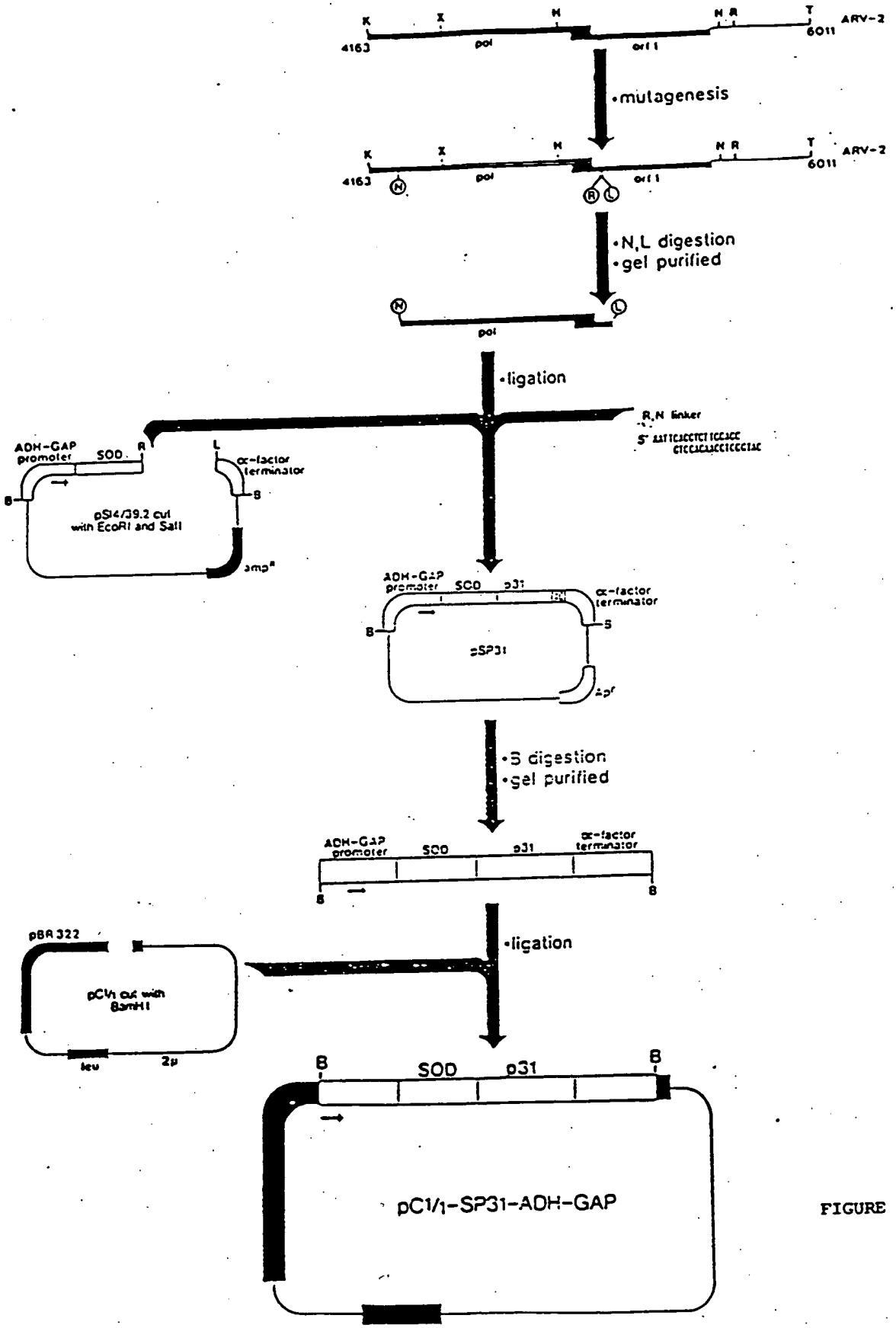



FIGURE 23

CONFIDENTIAL

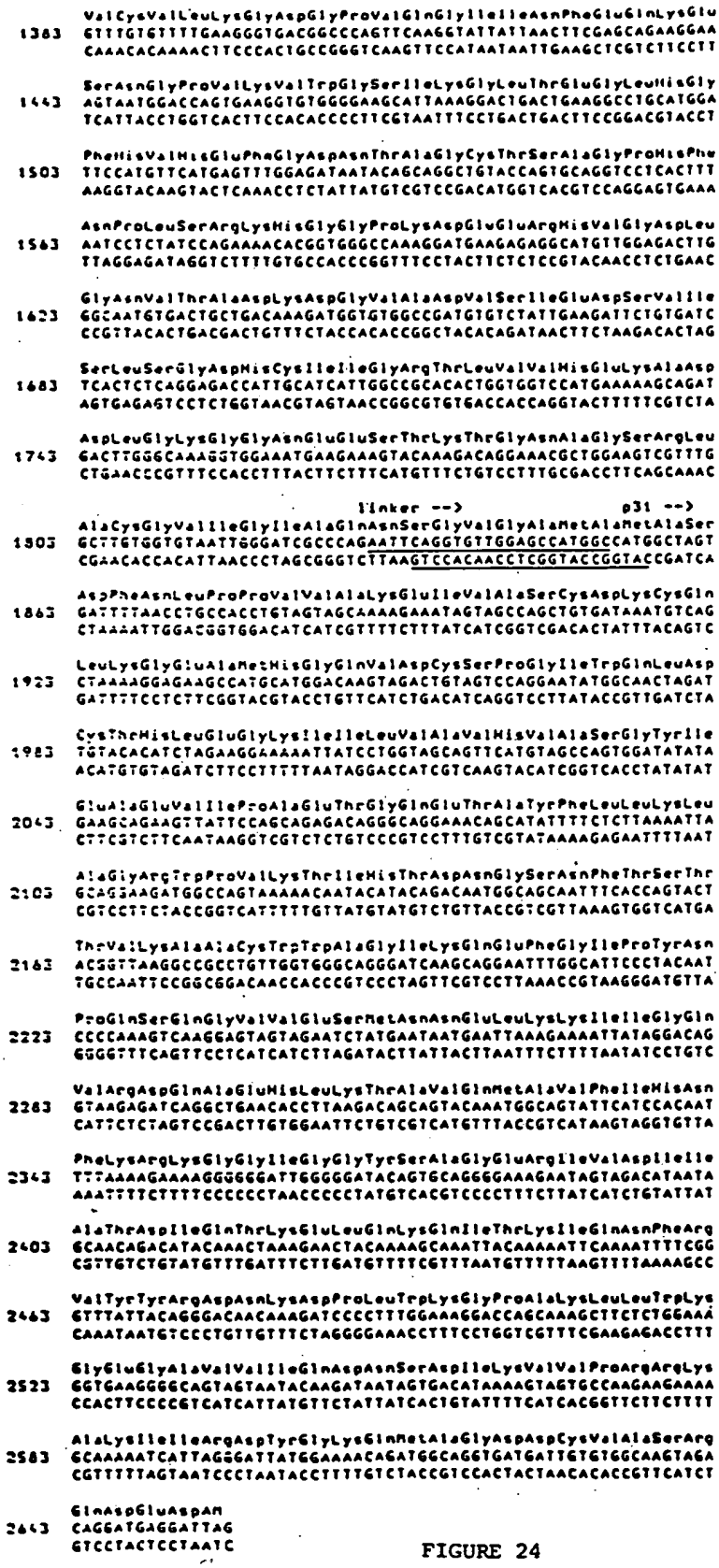



FIGURE 24

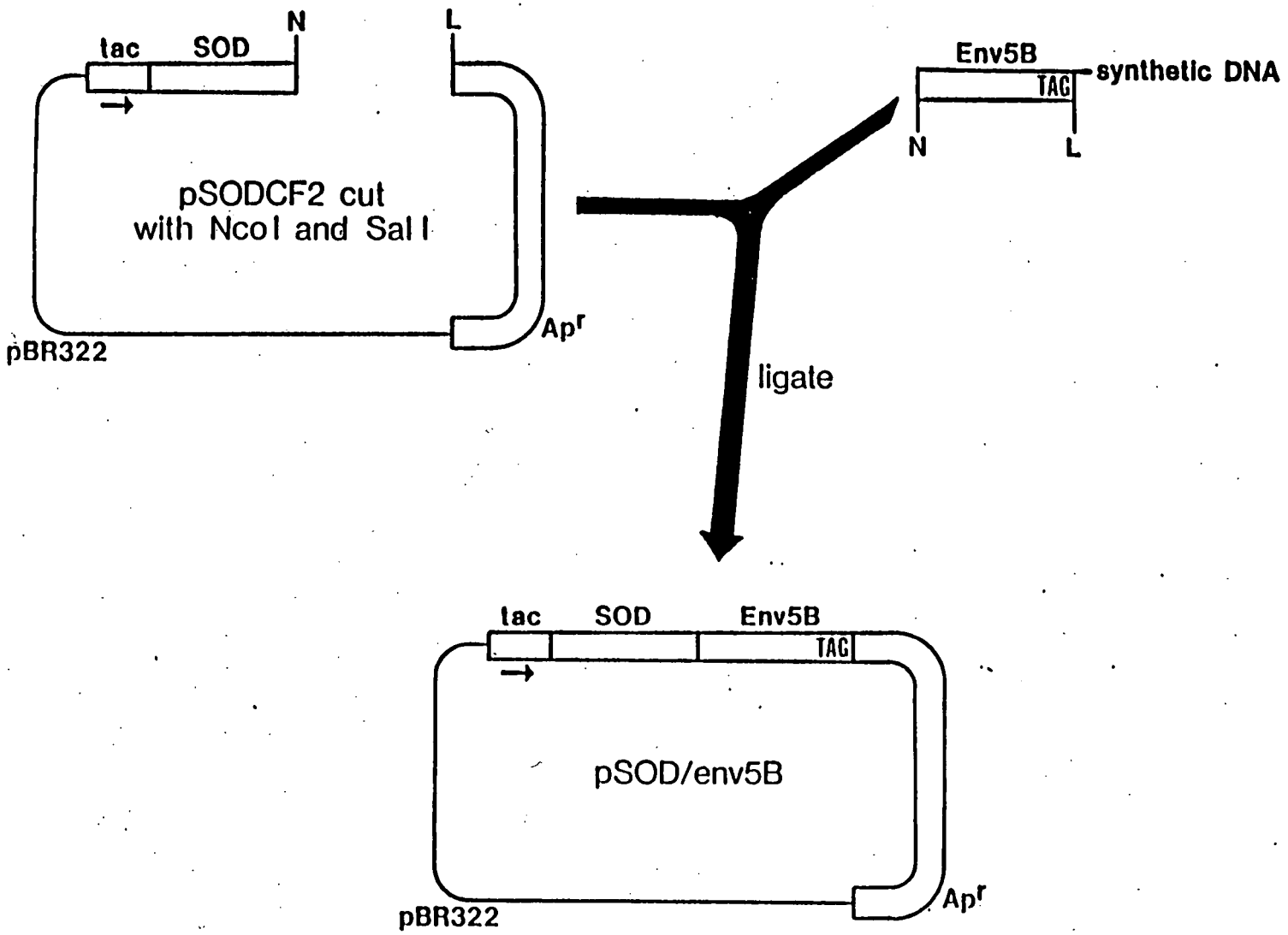
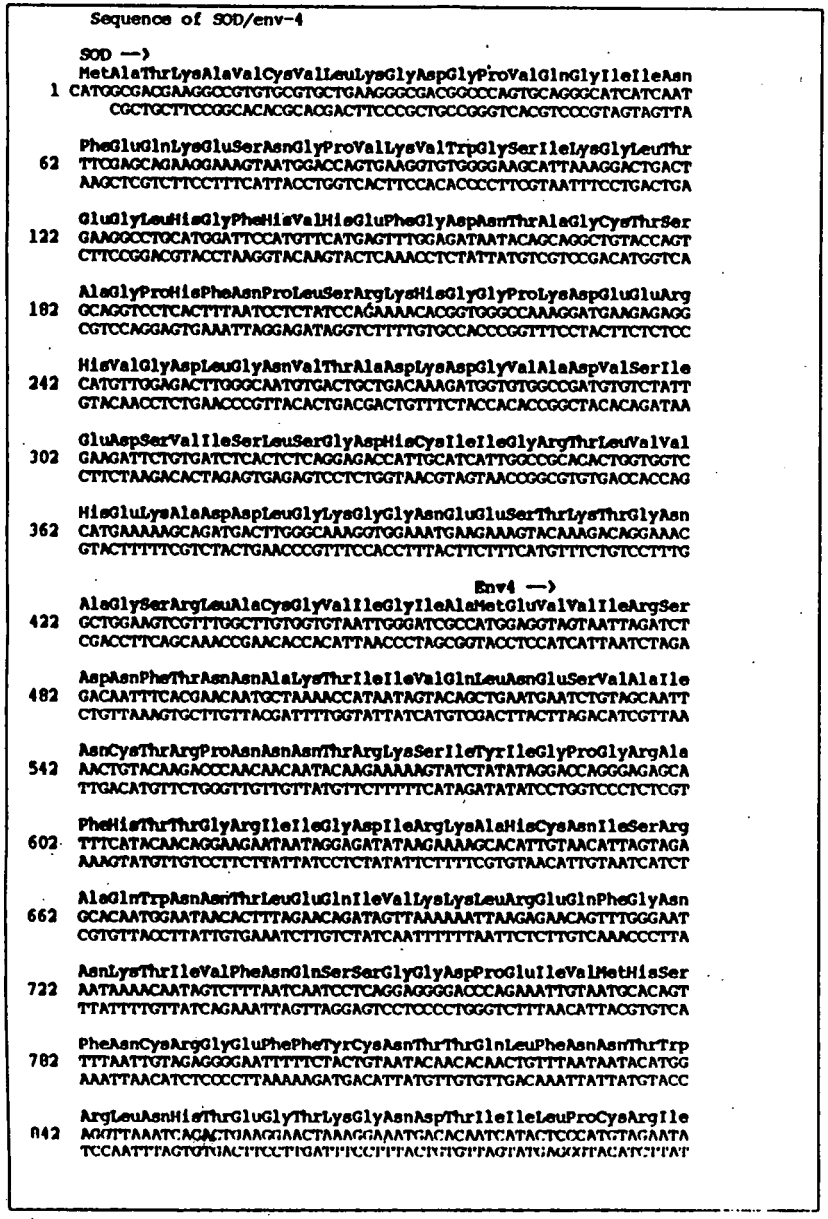


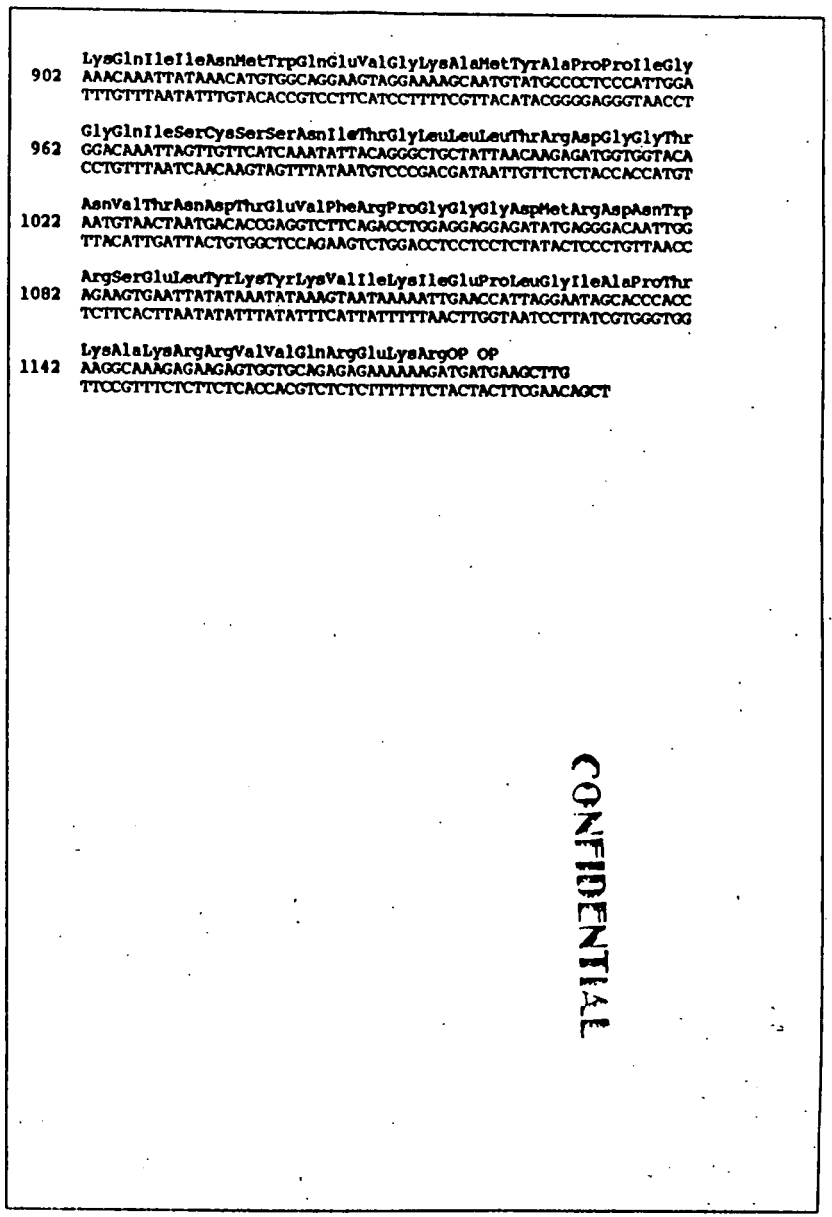

FIGURE 25

CONFIDENTIAL

08/288336

FIGURE 26




CONFIDENTIAL

08/288336

CONFIDENTIAL

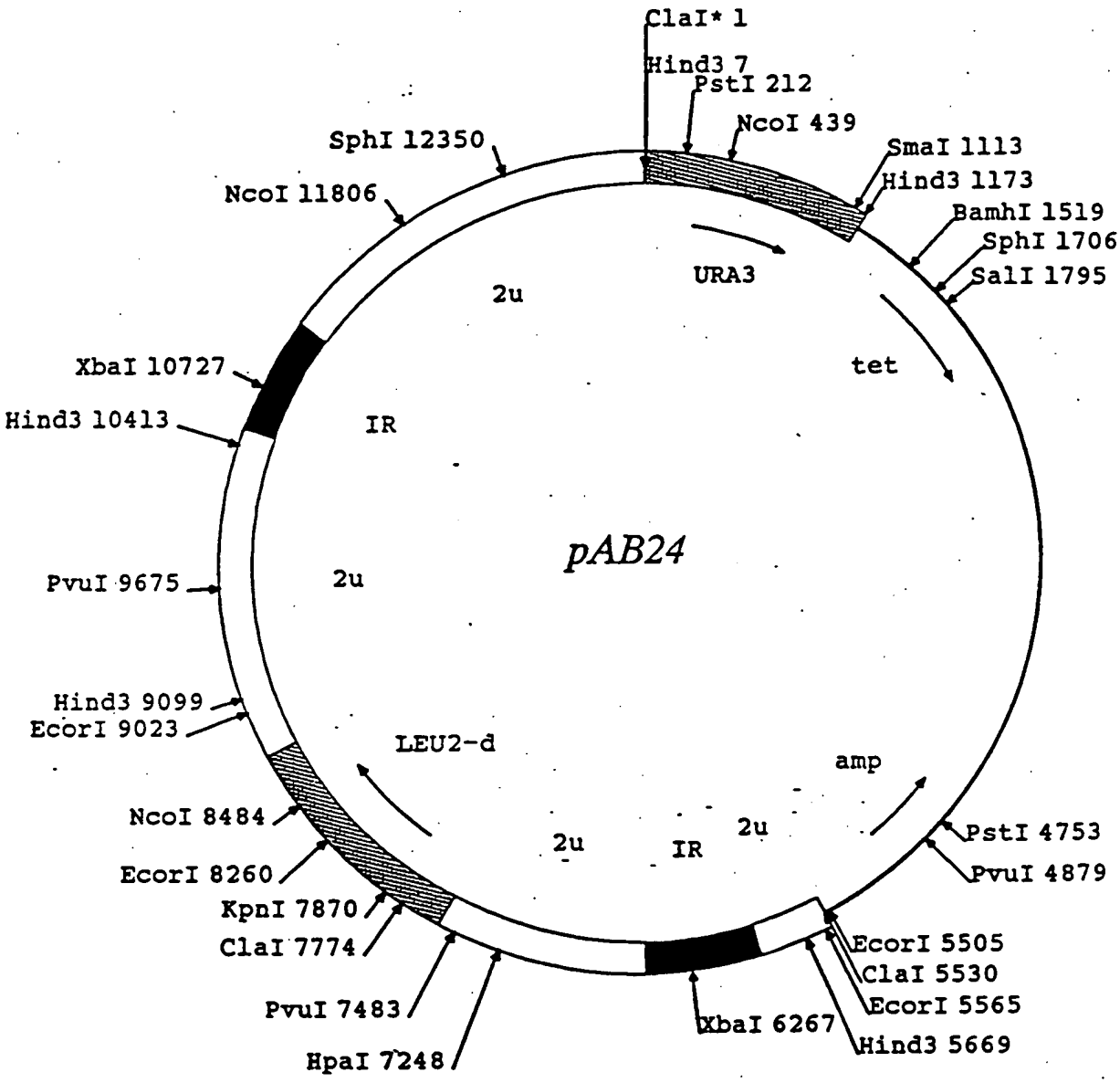



FIGURE 27

CONFIDENTIAL

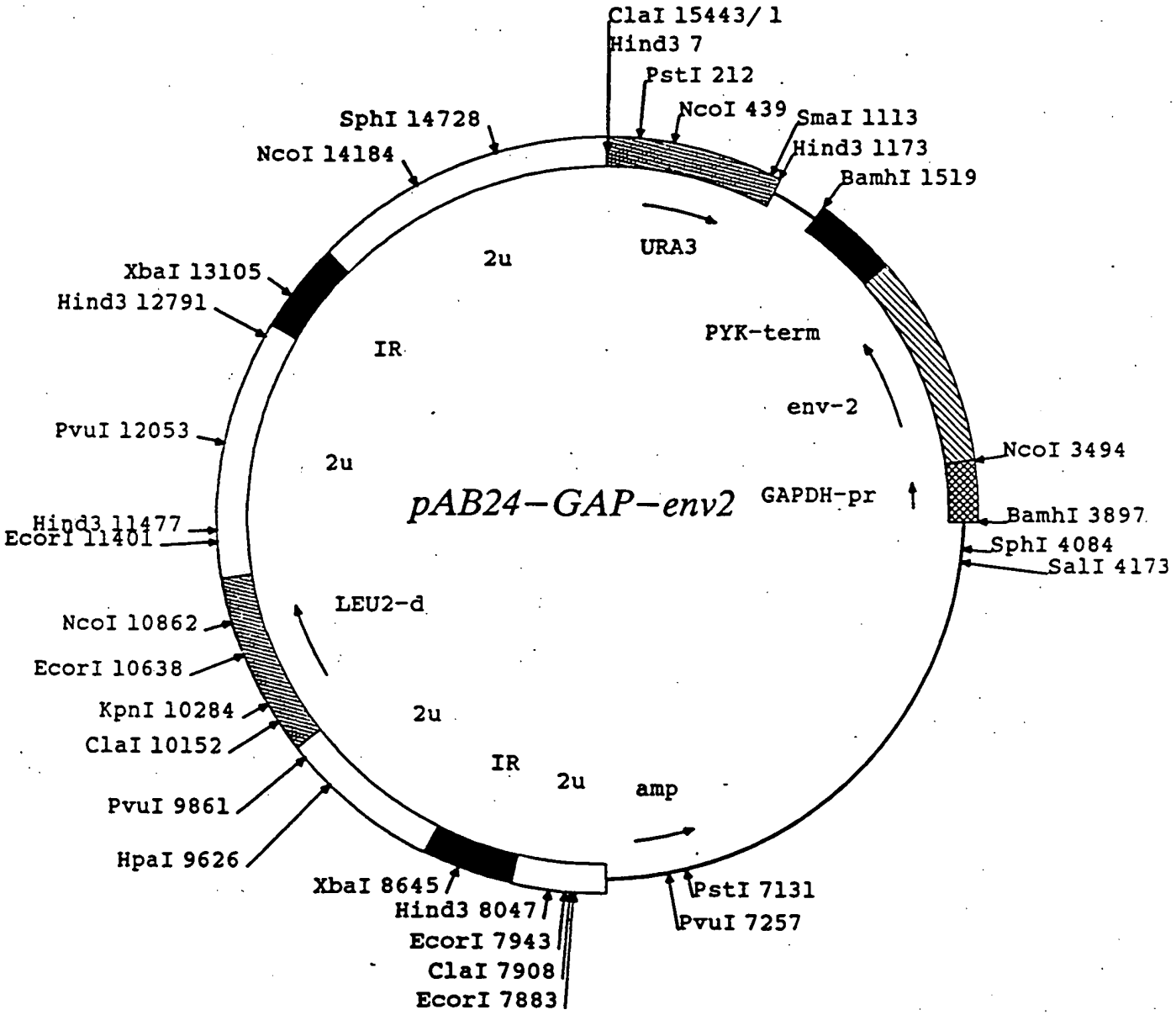



FIGURE 28

08/288336

CONFIDENTIAL

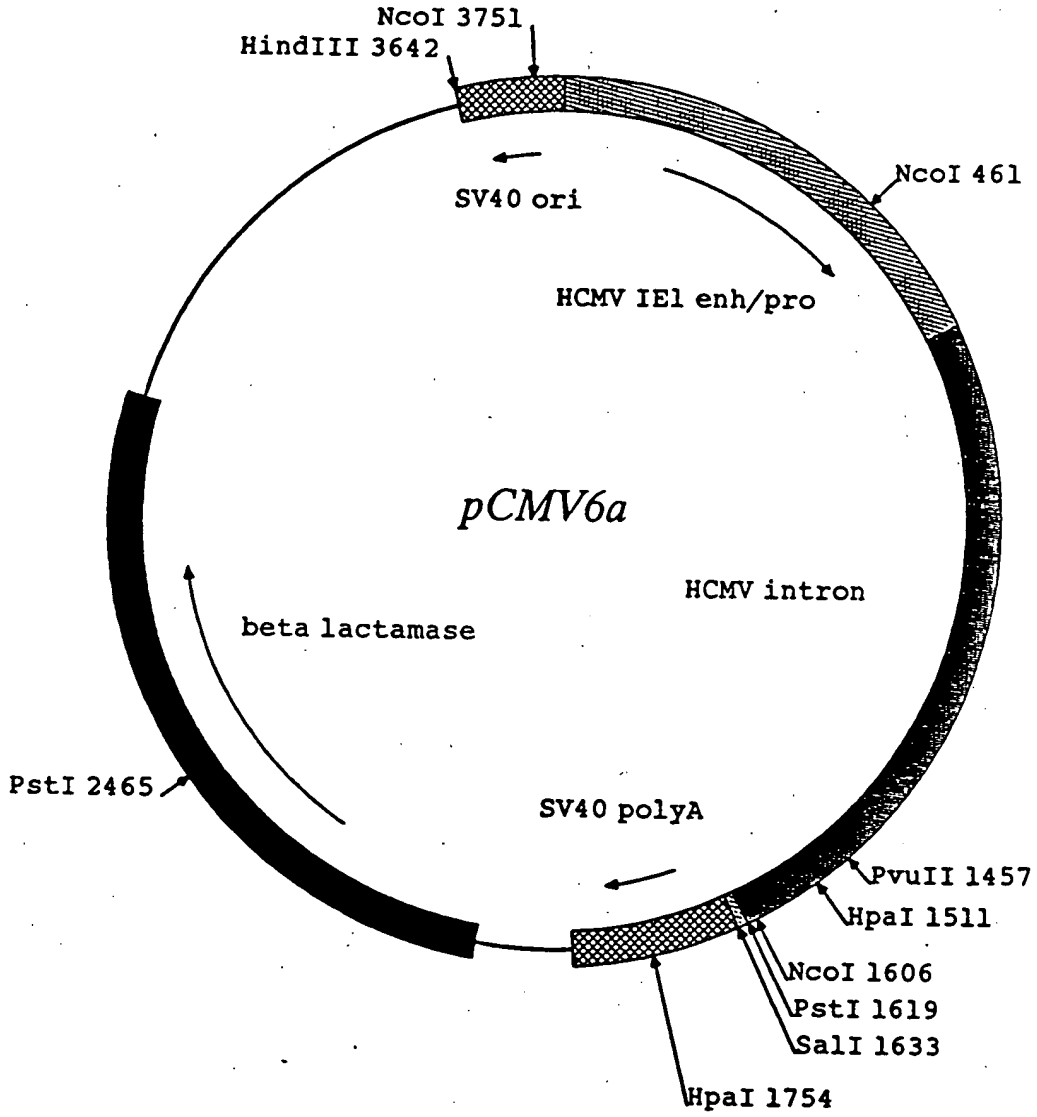



FIGURE 29

CONFIDENTIAL

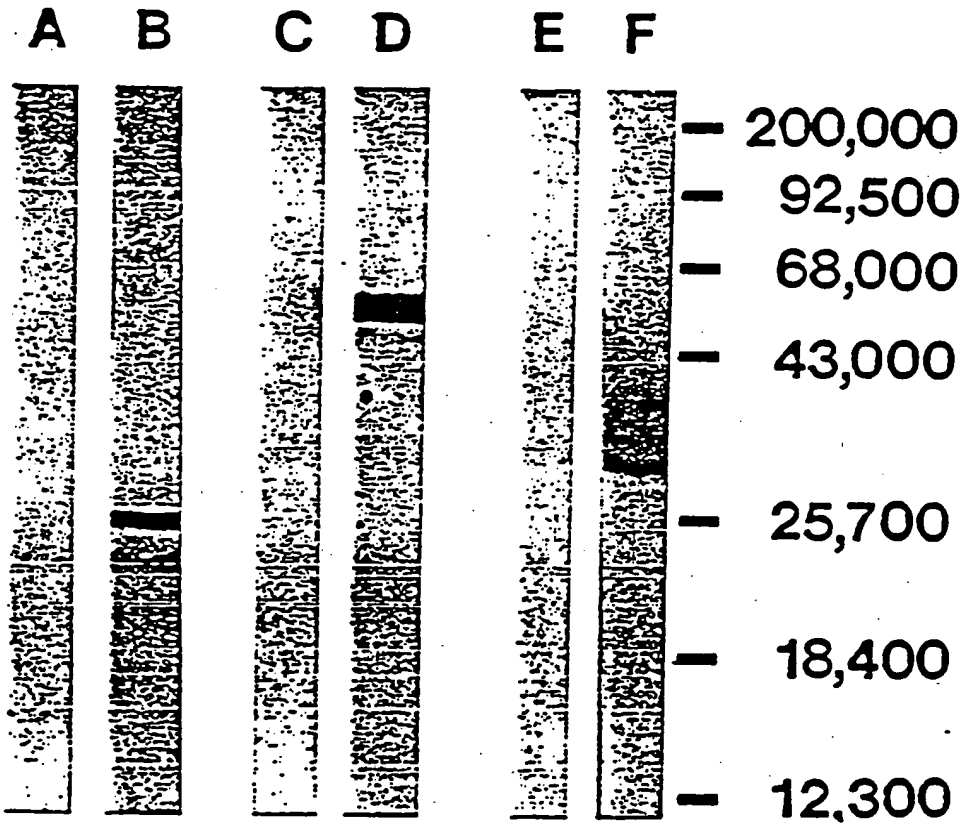



FIGURE 30